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(54) Title: ANTIBODIES THAT BLOCK RECEPTOR PROTEIN TYROSINE KINASE ACTIVATION, METHODS OF SCREENING FOR AND USES THEREOF

(57) Abstract: Molecules containing the antigen-binding portion of antibodies that block constitutive and/or ligand-dependent activation of a receptor protein tyrosine kinase, such as fibroblast growth factor receptor 3 (FGFR3), are found through screening methods, where a soluble dimeric form of a receptor protein tyrosine kinase is used as target for screening a library of antibody fragments displayed on the surface of bacteriophage. The molecules of the present invention which block constitutive activation can be administered to treat or inhibit skeletal dysplasia, craniosynostosis disorders, cell proliferative diseases or disorders, or tumor progression associated with the constitutive activation of a receptor protein tyrosine kinase.

ANTIBODIES THAT BLOCK RECEPTOR PROTEIN TYROSINE KINASE
ACTIVATION, METHODS OF SCREENING FOR AND USES THEREOF

Field of the Invention

5   The present invention relates to: immunoglobulins (and functional fragments thereof) useful
for blocking activation of receptor protein tyrosine kinases, methods for screening for such
immunoglobulins, compositions comprising said immunoglobulins and methods of using the
same for treating or inhibiting disease, such as skeletal dysplasia, craniosynostosis disorders,
cell proliferative diseases or disorders, or tumor progression.

10   **Background of the Invention**

A wide variety of biological processes involves complex cellular communication
mechanisms. One of the primary means of continual exchange of information between cells
and their internal and external environments is via the secretion and specific binding of
peptide growth factors. Growth factors exert pleiotropic effects and play important roles in
15   oncogenesis and the development of multicellular organisms regulating cell growth,
differentiation and migration. Many of these factors mediate their effects by binding to
specific cell surface receptors. The ligand-activated receptors start an enzymatic signal
transduction cascade from the cell membrane to the cell nucleus, resulting in specific gene
regulation and diverse cellular responses.

20   Protein Kinases

One of the key biochemical mechanisms of signal transduction involves the reversible
phosphorylation of proteins, which enables regulation of the activity of mature proteins by
altering their structure and function.

Protein kinases ("PKs") are enzymes that catalyze the phosphorylation of hydroxy groups on
25   tyrosine, serine and threonine residues of proteins. The consequences of this seemingly
simple activity are staggering; cell growth, differentiation and proliferation; e.g., virtually all
aspects of cell life in one way or another depend on PK activity. Furthermore, abnormal PK
activity has been related to a host of disorders, ranging from relatively non-life threatening
diseases such as psoriasis to extremely virulent diseases such as glioblastoma.

The kinases fall largely into two groups, those specific for phosphorylating serine and threonine, and those specific for phosphorylating tyrosine. Some kinases, referred to as "dual specificity" kinases, are able to phosphorylate tyrosine as well as serine/threonine residues.

Protein kinases can also be characterized by their location within the cell. Some kinases are

5   transmembrane receptor proteins capable of binding ligands external to the cell membrane. Binding the ligands alters the receptor protein kinase's catalytic activity. Others are non-receptor proteins lacking a transmembrane domain and yet others are ecto-kinases that have a catalytic domain on the extracellular (ecto) portion of a transmembrane protein or which are secreted as soluble extracellular proteins.

10   Many kinases are involved in regulatory cascades where their substrates may include other kinases whose activities are regulated by their phosphorylation state. Thus, activity of a downstream effector is modulated by phosphorylation resulting from activation of the pathway.

Receptor protein tyrosine kinases (RPTKs) are a subclass of transmembrane-spanning

15   receptors endowed with intrinsic, ligand-stimulatable tyrosine kinase activity. RPTK activity is tightly controlled. When mutated or altered structurally, RPTKs can become potent oncoproteins, causing cellular transformation. In principle, for all RPTKs involved in cancer, oncogenic deregulation results from relief or perturbation of one or several of the auto-control mechanisms that ensure the normal repression of catalytic domains. More than half

20   of the known RPTKs have been repeatedly found in either mutated or overexpressed forms associated with human malignancies (including sporadic cases; Blume-Jensen et al., 2001). RPTK over expression leads to constitutive kinase activation by increasing the concentration of dimers. Examples are Neu/ErbB2 and epidermal growth factor receptor (EGFR), which are often amplified in breast and lung carcinomas and the fibroblast growth factors (FGFR)

25   associated with skeletal and proliferative disorders (Blume-Jensen et al., 2001).

Fibroblast Growth Factors

Normal growth, as well as tissue repair and remodeling, require specific and delicate control of activating growth factors and their receptors. Fibroblast Growth Factors (FGFs) constitute a family of over twenty structurally related polypeptides that are developmentally regulated

30   and expressed in a wide variety of tissues. FGFs stimulate proliferation, cell migration and differentiation and play a major role in skeletal and limb development, wound healing, tissue repair, hematopoiesis, angiogenesis, and tumorigenesis (reviewed in Ornitz and Itoh, 2001).

The biological action of FGFs is mediated by specific cell surface receptors belonging to the RPTK family of protein kinases. These proteins consist of an extracellular ligand binding domain, a single transmembrane domain and an intracellular tyrosine kinase domain which undergoes phosphorylation upon binding of FGF. The FGF receptor (FGFR) extracellular

5   region contains three immunoglobulin-like (Ig-like) loops or domains (D1, D2 and D3), an acidic box, and a heparin binding domain. Five FGFR genes that encode for multiple receptor protein variants have been identified to date.

Another major class of cell surface binding sites includes binding sites for heparan sulfate proteoglycans (HSPG) that are required for high affinity interaction and activation of all

10   members of the FGF family. Tissue-specific expression of heparan sulfate structural variants confer ligand-receptor specificity and activity of FGFs.

FGFR-Related Disease

Recent discoveries show that a growing number of skeletal abnormalities, including achondroplasia, the most common form of human dwarfism, result from mutations in FGFRs.

15   Specific point mutations in different domains of FGFR3 are associated with autosomal dominant human skeletal disorders including hypochondroplasia, severe achondroplasia with developmental delay and acanthosis nigricans (SADDAN) and thanatophoric dysplasia (TD) (Cappellen et al., 1999; Webster et al., 1997; Tavormina et al.,1999). FGFR3 mutations have also been described in two craniosynostosis phenotypes: Muenke coronal craniosynostosis

20   (Bellus et al., 1996; Muenke et al., 1997) and Crouzon syndrome with acanthosis nigricans (Meyers et al., 1995). Crouzon syndrome is associated with specific point mutations in FGFR2 and both familial and sporadic forms of Pfeiffer syndrome are associated with mutations in FGFR1 and FGFR2 (Galvin et al., 1996; Schell et al., 1995). Mutations in FGFRs result in constitutive activation of the mutated receptors and increased receptor

25   protein tyrosine kinase activity, rendering cells and tissue unable to differentiate. Specifically, the achondroplasia mutation results in enhanced stability of the mutated receptor, dissociating receptor activation from down-regulation, leading to restrained chondrocyte maturation and bone growth inhibition (reviewed in Vajo et al., 2000).

There is accumulating evidence for mutations activating FGFR3 in various types of cancer.

30   Constitutively activated FGFR3 in a large proportion of two common epithelial cancers, bladder and cervix, as well as in multiple myeloma, is the first evidence of an oncogenic role for FGFR3 in carcinomas. FGFR3 currently appears to be the most frequently mutated

- 3 -

oncogene in bladder cancer where it is mutated in almost 50% of the cases and in about 70% of cases having recurrent superficial bladder tumors (Cappellen, et al, 1999; van Rhijn, et al, 2001; Billerey, et al, 2001). FGFR3 mutations are seen in 15-20% of multiple myeloma cases where point mutations that cause constitutive activation directly contribute to tumor

5   development and progression (Chesi, et al, 1997; Plowright, et al, 2000, Ronchetti, et al, 2001).

In this context, the consequences of FGFR3 signaling appear to be cell type-specific. In chondrocytes, FGFR3 hyperactivation results in growth inhibition (reviewed in Ornitz, 2001), whereas in the myeloma cell it contributes to tumor progression (Chesi et al., 2001).

10   In view of the link between RPTK-related cellular activities and a number of human disorders various strategies have been employed to target the receptors and/or their variants for therapy. Some of these have involved biomimetic approaches using large molecules patterned on those involved in the cellular processes, e.g., mutant ligands (US Patent 4,966,849); soluble receptors and antibodies (WO 94/10202, US 6,342,219); RNA ligands

15   (US Patent 5,459,015) and tyrosine kinase inhibitors (WO 94/14808; US Patent 5,330,992).

Antibody therapy

The search for new therapies to treat cancer and other diseases associated with growth factors and their corresponding cell surface receptors has resulted in the development of humanized antibodies capable of inhibiting receptor function. For example, US patents 5,942,602 and

20   6,365,157 disclose monoclonal antibodies specific for the HER2/neu and VEGF receptors, respectively. US patent 5,840,301 discloses a chimeric, humanized monoclonal antibody that binds to the extracellular domain of VEGF and neutralizes ligand-dependent activation.

There is an unmet need for highly selective molecules capable of blocking aberrant constitutive receptor protein tyrosine kinase activity, in particular FGFR activity, thereby

25   addressing the clinical manifestations associated with the above-mentioned mutations, and modulating various biological functions.

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30   information available to applicant at the time of filing and does not constitute an admission as to the correctness of such a statement.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide molecules which are able to block receptor protein tyrosine kinase (RPTK) activity.

It is an object of the present invention to provide molecules which are able to block fibroblast growth factor receptor (FGFR) activity, and more preferably fibroblast growth factor receptor 3 (FGFR3) activity.

It is another object of the present invention to provide a method to screen for molecules which are able to block said receptor activity.

It is yet another object of the present invention to provide a pharmaceutical composition comprising as an active ingredient a molecule of the invention useful in treating or preventing skeletal and proliferative diseases and disorders.

It is a further object of the present invention to provide a method for inhibiting growth of tumor cells associated with ligand-dependent or constitutive activation of a receptor protein tyrosine kinase, preferably a fibroblast growth factor receptor, and more preferably FGFR3.

It is yet a further object of the present invention to provide a method for treating skeletal disorders associated with ligand-dependent or constitutive activation of a receptor protein tyrosine kinase, preferably a fibroblast growth factor receptor, and more preferably FGFR3.

It is yet a further object of the present invention to provide a method for blocking receptor protein tyrosine kinase activation in the cells of patients in need thereof by treatment with molecules capable of inhibiting receptor protein tyrosine kinase function.

It is yet another object of the present invention to provide a method for inhibiting tumor growth, tumor progression or metastases.

It is still a further object to provide molecules useful for in vivo imaging of diseased states.

It is still a further object of the invention to provide a kit containing molecules of the invention.

These and other objects are met by the invention disclosed herein.

The present invention provides a molecule that contains the antigen-binding portion of an antibody which has a specific affinity for a receptor protein tyrosine kinase and which blocks constitutive activation of a receptor protein tyrosine kinase. The present invention further

provides a molecule that contains the antigen-binding portion of an antibody which has a specific affinity for a receptor protein tyrosine kinase and which blocks ligand-dependent activation of a fibroblast growth factor receptor (FGFR), including FGFR1 and FGFR3.

Certain molecules of the present invention were found to inhibit or block constitutive, or ligand independent, activation of the FGFR3. Generation of inhibitory molecules would be useful for developing medicaments for use in treating or preventing skeletal and proliferative diseases and disorders associated with constitutive activation of receptor protein tyrosine kinases.

Certain mutations in the genes of receptor protein tyrosine kinases result in activation of the receptor in a manner that is independent of the presence of a ligand. Such ligand-independent, or constitutive, receptor protein tyrosine kinase activation results in increased receptor activity. The clinical manifestations of certain mutations are skeletal and proliferative disorders and diseases, including achondroplasia and various cancers.

Furthermore, the present invention is directed to novel molecules comprising an antigen binding domain which binds to a receptor protein tyrosine kinase and blocks constitutive activation of said receptor protein tyrosine kinase. The molecules of the invention maybe antibodies or antigen binding fragments thereof.

A currently preferred embodiment of the present invention provides a molecule which binds to the extracellular domain of a receptor protein tyrosine kinase and blocks constitutive and ligand-dependent activation of the receptor.

A currently more preferred embodiment of the present invention provides a molecule which binds to the extracellular domain of an FGF receptor and blocks constitutive and ligand-dependent activation of the receptor.

A currently most preferred embodiment of the present invention provides a molecule which binds FGFR3 and blocks constitutive and ligand-dependent activation of the receptor, comprising V_L-CDR3 and V_H-CDR3 regions having SEQ ID NO:25 and 24, respectively and the corresponding polynucleotide sequence SEQ ID NO:51 and 50.

A currently most preferred embodiment of the present invention provides a molecule which binds FGFR3 and blocks constitutive and ligand-dependent activation of the receptor, comprising V_L-CDR3 and V_H-CDR3 regions having SEQ ID NO:13 and 12 or SEQ ID NO:9

and 8, respectively and the corresponding polynucleotide sequence SEQ ID NO:35 and 34 or SEQ ID NO: 31 and 30.

Another currently preferred embodiment of the present invention provides a molecule herein denoted MSPRO12 comprising a light chain having SEQ ID NO:94 and a heavy chain having

5   SEQ ID NO:105 and the corresponding polynucleotide sequences having SEQ ID NO:75 and 89, respectively.

Another currently preferred embodiment of the present invention provides a molecule herein denoted MSPRO2 comprising a light chain having SEQ ID NO:92 and a heavy chain having SEQ ID NO:103 and the corresponding polynucleotide sequences having SEQ ID NO:74

10   and 86,

Another currently most preferred embodiment of the present invention provides a molecule herein denoted MSPRO59 comprising a light chain having SEQ ID NO:102 and a heavy chain having SEQ ID NO:113 and the corresponding polynucleotide sequences having SEQ ID NO:76 and 91, respectively.

15   According to the principles of the present invention, molecules which bind FGFR and block ligand-dependent receptor activation are provided. These molecules are useful in treating disorders and diseases associated with an FGFR that is activated in a ligand-dependent manner including certain skeletal disorders, hyperproliferative diseases or disorders and non-neoplastic angiogenic pathologic conditions such as neovascular glaucoma, macular

20   degeneration, hemangiomas, angiofibromas, psoriasis and proliferative retinopathy including proliferative diabetic retinopathy.

A currently most preferred embodiment of the present invention provides a molecule which binds FGFR3 and blocks ligand-dependent activation of the receptor, comprising V_H-CDR3 and V_L-CDR3 regions having SEQ ID NO:20 and 21 , respectively and the corresponding

25   polynucleotide sequence SEQ ID NO:44 and 45, respectively.

Other currently preferred embodiments of the present invention provides a molecule which binds FGFR3 and blocks ligand-dependent activation of the receptor, comprising V_H-CDR3 and V_L-CDR3 regions selected from the group consisting of SEQ ID NO:10 and SEQ ID NO:11; SEQ ID NO:14 and SEQ ID NO:15; SEQ ID NO:16 and SEQ ID NO:17; SEQ ID

30   NO:18 and SEQ ID NO:19; SEQ ID NO:20 and SEQ ID NO:21; SEQ ID NO:26 and SEQ ID NO:27 or SEQ ID NO:28 and SEQ ID NO:29 and the corresponding polynucleotide sequences according to table 1B.

Additional currently preferred embodiments of the present invention provide molecules having an antigen binding domain comprising a VL region and a VH region, respectively, selected from the group consisting of respectively, selected from the group consisting of SEQ ID NO: 92 and 103; SEQ ID NO: 93 and 104; SEQ ID NO: 94 and 105; SEQ ID NO:95 and

5   106; SEQ ID NO: 96 and 107 ; SEQ ID NO: 97 and 108; SEQ ID NO:98 and 109; SEQ ID NO: 99 and 110; SEQ ID NO: 101 and 112; and SEQ ID NO:102 and 113.

A currently preferred embodiment of the present invention provides a molecule comprising V_H-CDR3 and V_L-CDR3 domains having SEQ ID NO:22 and SEQ ID NO:23, which has specific affinity for FGFR1 and which blocks ligand-dependent activation of FGFR1, and the

10   corresponding polynucleotides having SEQ ID NO:46 and SEQ ID NO:47.

A currently preferred embodiment of the present invention provides a molecule comprising domains having SEQ ID NO: 100 and 111, which has specific affinity for FGFR1 and which blocks ligand-dependent activation of FGFR1, and the corresponding polynucleotides having SEQ ID NO:73 and SEQ ID NO:82.

15   In addition, the present invention also relates to methods for screening for the molecules according to the present invention by using a dimeric form of a receptor protein tyrosine kinase as a target for screening a library of antibody fragments.

According to one currently preferred embodiment the screening method comprises

screening a library of antibody fragments for binding to a dimeric form of a receptor

20   protein tyrosine kinase;

identifying an antibody fragment which binds to the dimeric form of the receptor protein tyrosine kinase as a candidate molecule for blocking constitutive activation of the receptor protein tyrosine kinase; and

determining whether the candidate molecule blocks constitutive or ligand-dependent

25   activation of the receptor protein tyrosine kinase in a cell.

According to another currently preferred embodiment the dimeric form of the RPTK is a soluble extracellular domain of a receptor protein tyrosine kinase. Non-limiting examples of receptor protein tyrosine kinases disclosed in Blume-Jensen et al. (2001) include EGFR/ErbB1, ErbB2/HER2/Neu, ErbB/HER3, ErbB4/HER4, IGF-1R, PDGFR-α, PDGFR-β,

30   CSF-1R, kit/SCFR, Flk2/FH3, Flk1/VEGFR1, Flk1/VEGFR2, Flt4/VEGFR3, FGFR1,

FGFR2/K-SAM, FGFR3, FGFR4, TrkA, TrkC, HGFR, RON, EphA2, EphB2, EphB4, Axl, TIE/TIE1, Tek/TIE2, Ret, ROS, Alk, Ryk, DDR, LTK and MUSK.

By using a dimeric form of the RPTK as bait in the screen, a molecule which would bind to the dimeric form of the receptor has been identified. This presents a novel concept in

5   screening for antibodies or fragments thereof with the capacity to bind to a constitutively activated RPTK such as those associated with various disorders and diseases. It also presents an opportunity to screen for molecules which bind to a heterodimer RPTK. A further aspect of the present invention provides a pharmaceutical composition comprising as an active ingredient a molecule of the present invention useful for preventing or treating skeletal or

10   cartilage diseases or disorders and craniosynostosis disorders associated with constitutive or ligand-dependent activation of a receptor protein tyrosine kinase.

In a currently preferred embodiment the pharmaceutical compositions of the present invention may be used for treating or preventing skeletal disorders associated with aberrant FGFR signaling, including achondroplasia, thanatophoric dysplasia, Apert or Pfeiffer

15   syndrome and related craniosynostosis disorders.

A further aspect of the present invention provides a pharmaceutical composition comprising as an active ingredient a molecule of the present invention useful for preventing or treating cell proliferative diseases or disorders or tumor progression, associated with the constitutive or ligand-dependent activation of a receptor protein tyrosine kinase.

20   In a currently preferred embodiment the pharmaceutical compositions of the present invention may be used for treating or preventing proliferative diseases associated with aberrant FGFR signaling, including multiple myeloma, transitional cell carcinoma of the bladder, mammary and cervical carcinoma, chronic myeloid leukemia and osteo- or chondrosarcoma.

25   A further aspect of the invention provides molecules comprising an antigen binding domain which can be conjugated to cytotoxins useful for targeting cells expressing said antigen.

Another currently preferred aspect of the present invention provides molecules comprising an antigen binding domain which can be conjugated to appropriate detectable imaging moiety, useful for in vivo tumor imaging.

30   A still further aspect of the present invention provides methods for treating or inhibiting the aforementioned diseases and disorders by administering a therapeutically effective amount of

a pharmaceutical composition comprising a molecule of the present invention to a subject in need thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows hFR3$^{23-374}$TDhis purification by Coommassie stained SDS-PAGE.

Figure 2 shows hFR3$^{23-374}$TDhis binding to heparin and FGF9.

Figure 3 shows the purification of FR3exFc and FR1exFc on SDS-PAGE.

5   Figure 4 shows the neutralization effect of the hFR3$^{23-374}$TDhis and FR3exFc soluble receptors in a ligand-dependent proliferation assay.

Figure 5 shows the effect of MSPRO Fabs on proliferation of FGFR1 and FGFR3-expressing cells.

Figure 6 shows the effect of MSPRO Fabs on proliferation of FGFR3-expressing cells.

10   Figures 7A and 7B show the neutralizing activity of several MSPRO Fabs in a proliferation assay using the FDCP-FR3 (C10; Fig. 7A) or the FDCP-FR1 cells (Fig. 7B).

Figure 8 shows the receptor specificity of MSPRO Fabs on RCJ-FR3 cells by Western blot using an anti-P-ERK antibody. Figure 8A shows different MSPRO Fabs while Figure 8B shows a dose response of MSPRO 12, 29 and 13 on RCJ-FR3 cells.

15   Figures 9A-9D demonstrates the specificity and potency of MS-PRO Fabs by Western blot with anti-P-ERK antibody.

Figure 10 shows a diagrammatic representation of FGFR3 and of FGFR3 truncations (D2-3, D2) and isoforms (IIIb, IIIc). The isoform IIIb differs from IIIc at the carboxy terminus of the IgIII domain as indicated with a dotted line.

20   Figure 11 shows that the FGFR3 neutralizing Fabs recognize IgII or IgII and III in the extracellular region of FGFR3.

Figure 12 shows that MSPRO29 specifically recognizes the IIIc isoform of FGFR3.

Figure 13 shows the results of a proliferation assay for FDCP-FR3IIIb or FDCP-FR3IIIc cells incubated with increasing dose of the indicated Fabs.

25   Figure 14 shows iodinated MSPRO29 binding to FGFR3.

Figure 15 shows results of a proliferation assay is a graph wherein iodinated MSPRO29 retained its activity against FGFR3.

Figures 16A-16F show the selective binding of radiolabelled MS-PRO29 to histological of growth plate.

Figure 17 shows a proliferation assay of FDCP-FR3 (C10) and FDCP-FR3ach cells incubated with FGF9 and with increasing doses of the indicated Fabs.

Figure 18B shows that MSPRO12 and MSPRO59 inhibit the ligand independent proliferation of FDCP-FR3ach cells. Fig. 18A shows analysis of the ligand-dependent FDCP-FR3wt cells.

Figure 19 shows the restoration of cell growth in RCS cells by MS-PRO54 and MSPRO59..

Figure 20 represents the growth rate of treated bone with MS-PRO 59.

Figure 21 is a flow chart of the experimental protocol for assessing receptor activation and signaling.

Figure 22 shows ^{125}I labeled MSPRO59 localization to the FDCP-FR3ach derived tumor.

Figure 23 shows the effect of MSPRO59 on inhibiting ligand-independent tumor growth after 24 and 26 days.

Figure 24 shows the effect of MSPRO59 on inhibiting ligand-independent tumor growth.

Figure 25A shows the effect of MSPRO59 on inhibiting ligand-independent tumor growth. Figure 25B shows scFv MSPRO59 blocking the proliferation of FDCP-FR3 (S375C) cells.

Figure 26 shows the effect of MSPRO59 single chain antibody on inhibiting ligand-independent tumor growth.

Figure 27 shows binding of Fab Miniantibodies to FGFR3-Fc and FGFR1-Fc (ELISA).

Figure 28A is an example of a Fab expression vector for use in accordance with the present invention.

Figure 28B is the DNA sequence of the vector according to Figure 28A

Figure 29A is an example of a phage display vector for use in accordance with the present invention.

Figure 29B is the DNA sequence of the vector according to Figure 29A.

Figure 30 depicts the polynucleotide sequences of the VL and VH of MSPRO antibodies of the present invention.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based on the discovery that neutralizing antibodies that block ligand-dependent and ligand-independent activation of fibroblast growth factor 3 (FGFR3), a

5   receptor protein tyrosine kinase (RPTK), can be obtained by screening an antibody library against a dimeric form of the extracellular portion of FGFR3. Until the present invention, the present inventors are unaware of any success in obtaining neutralizing antibodies that block constitutive activation of any RPTK including FGFR or ligand-dependent FGFR activation.

The term "receptor protein tyrosine kinase" or "RPTK" as used herein and in the claims

10   refers to a subclass of transmembrane-spanning receptors endowed with intrinsic, ligand-stimulatable tyrosine kinase activity. RPTKs comprise a large family of spatially and temporally regulated proteins that control many different aspects of growth and development. When mutated or altered structurally, RPTKs can undergo deregulation and become activated in a ligand-independent, or constitutive, manner. In certain cases they become potent

15   oncoproteins, causing cellular transformation.

As used herein and in the claims the term "fibroblast growth factor receptor" or "FGFR" denotes a receptor specific for FGF which is necessary for transducing the signal exerted by FGF to the cell interior, typically comprising an extracellular ligand-binding domain, a single transmembrane helix, and a cytoplasmic domain having tyrosine kinase activity. The FGFR

20   extracellular domain consists of three immunoglobulin-like (Ig-like) domains (D1, D2 and D3), a heparin binding domain and an acidic box. Alternative splicing of the FGF receptor mRNAs generates different variants of the receptors.

Molecules, including antibodies and fragments thereof, comprising an antigen binding domain to a receptor protein tyrosine kinase are highly necessary for the treatment of various

25   pathological conditions.

In the past, the laboratory of the present inventors encountered difficulties in raising neutralizing antibodies against FGFR3. When mice were immunized with the soluble monomeric FGFR3 receptor, by the time the antibody titers begins to increase, the mice died. The experiments performed in the laboratory of the present inventors that failed to obtain

30   anti-FGFR3 neutralizing antibodies in mice are presented in the Examples.

By using a soluble dimeric form of the extracellular domain of the FGFR3 receptor to screen for antibodies, e.g., Fabs, that bind from a phage display antibody library, the present inventors were able to overcome a problem in the prior art for which there was yet no solution and to obtain numerous high affinity (K_D < 10 nM) antibodies (Fabs) that bind

5   FGFR3 and interfere with ligand binding, thereby blocking ligand-dependent activation of FGFR3 signaling. Very surprisingly, from among the group of Fabs that block ligand-dependent activation, Fab antibodies which also block ligand-independent (constitutive) activation of FGFR3 by blocking signaling caused by constitutive dimerization of FGFR3 were identified. To the best of the present inventors' knowledge, the Fab antibodies obtained

10   which block constitutive activation of FGFR3 are the first antibodies against any receptor protein tyrosine kinase that blocks constitutive, ligand-independent activation/signaling.

Trastuzamab, an anti-human epidermal growth factor receptor 2 (HER2) antibody, was the first humanized monoclonal antibody approved for therapeutic use. Its mode of action appears to be manifold, including HER2 down regulation, prevention of heterodimer

15   formation, prevention of HER2 cleavage and others (Baselga and Albanell, 2001). US patents 5, 677171; 5772997; 6165464 and 6,399,063 disclose the anti-HER2 invention but neither teach nor suggest that the antibody blocks ligand-independent receptor activation.

One aspect of the present invention is directed to neutralizing antibodies and more generally to a molecule that includes the antigen binding portion of an antibody which blocks ligand-

20   dependent activation and constitutive, ligand-independent activation of a receptor protein tyrosine kinase, preferably an FGFR and more preferably FGFR3.

Another aspect of the present invention is directed to molecules comprising an antigen binding domain which blocks ligand-dependent activation of an FGFR, more preferably FGFR3.

25   The molecule having the antigen-binding portion of an antibody according to the present invention can be used in a method for blocking the ligand-dependent activation and/or ligand independent (constitutive) activation of FGFR3. Preferred embodiments of such antibodies/molecules, obtained from an antibody library designated as HuCAL® (Human Combinatorial Antibody Library) clone, is presented in Table 1 with the unique VH-CDR3

30   and VL-CDR3 sequences given.

In addition to sequencing of the clones, a series o biochemical assays were performed to determine affinity and specificity of the molecules to the respective receptors.

TABLE 1A

HuCAL® Clone	VH-CDR3 Sequence	VL-CDR3 equence	Framework
MSPRO2	DFLGYEFDY (SEQ ID NO: 8)	QSYDYSADY (SEQ IDNO: 9)	VH1B_L3
MSPRO11	YYGSSLYHYVFGGFIDY (SEQ ID NO: 10)	QSHHFYE (SEQ ID NO: 11)	VH1B_L2
MSPRO12	YHSWYEMGYYGSTVGYMFD (SEQ ID NO: 12)	QSYDFDFA (SEQ ID NO: 13)	VH2_L3
MSPRO21	DNWFKPFSDV (SEQ ID NO: 14)	QQYDSIPY (SEQ ID NO: 15)	VH1A_k4
MSPRO24	VNHWTYTFDY (SEQ ID NO: 16)	QQMSNYPD (SEQ ID NO: 17)	VH1A_k3
MSPRO26	GYWYAYFTYINYGYFDN (SEQ ID NO: 18)	QSYDNNSDV (SEQ ID NO: 19)	VH1B_L2
MSPRO28	GGGWVSHGYYYLFDL (SEQ ID NO: 26)	FQYGSIPP (SEQ ID NO: 27)	VH1A_k1
MSPRO29	TWQYSYFYYLDGGYYFDI (SEQ ID NO: 20)	QQTNNAPV (SEQ ID NO:21)	VH1B_k3
MSPRO54	NMAYTNYQYVNMPHFDY (SEQ ID NO: 22)	QSYDYFKL (SEQ ID NO:23)	VH1B_L3
MSPRO55	SMNSTMYWYLRRVLFDH (SEQ ID NO: 28)	QSYDMYMYI (SEQ ID NO: 29)	VH1B_L2
MSPRO59	SYYPDFDY (SEQ ID NO:24)	QSYDGPDLW (SEQ ID NO:25)	VH6_L3

VH refers to the variable heavy chain, VL refers to the variable light chain; L refers to the lambda light chain and k refers to the kappa light chain

Table 1B lists the corresponding polynucleotide sequences of the CDR domains.

5

TABLE 1B

HuCAL® Clone	VH-CDR3 polynucleotide sequence	VL-CDR3 polynucleotide Sequence
MSPRO2	GATTTTCTTGGTTATGAGTTTGATTAT (SEQ ID NO:30)	CAGAGCTATGAC TATTCTGCT GAT TAT (SEQ ID NO:31)
MSPRO11	TATTATGGTTCTTCTCTTTATCATTATGTTT TTGGTGGTTTTATTGATTAT (SEQ ID NO:32)	CAGTCTCATCAT TTTTATGAG (SEQ ID NO:33)
MSPRO12	TATCATTCTTGGTATGAGATGGGTTATTAT GGTTCTACTGTTGGTTATATGTTTGATTAT (SEQ ID NO:34)	CAGAGCTATGAC TTTGATTTT GCT (SEQ ID NO:35)
MSPRO21	GATAATTGGTTTAAGCCTTTTTCTGATGTT (SEQ ID NO:36)	CAGCAGTATGAT TCTATTCCT TAT (SEQ ID NO:37)
MSPRO24	GTTAATCATTGGACTTATACTTTTGATTAT (SEQ ID NO:38)	CAGCAGATGTCT AATTATCCTGAT (SEQ ID NO:39)
MSPRO26	GGTTATTGGTATGCTTATTTTACTTAT ATTAATTATGGTTATTTT GATAAT (SEQ ID NO:40)	CAGAGCTATGAC AATAATTCTGAT GTT (SEQ ID NO:41)
MSPRO28	GGTGGTGGTTGGGTTTCTCATGGTTATTAT TATCTTTTTGATCTT (SEQ ID NO:42)	TTTCAGTATGGT TCTATTCCT CCT (SEQ ID NO: 43)
MSPRO29	ACTTGGCAGTATTCTTATTTTTATTAT CTTGATGGTGGTTATTATTTTGATATT (SEQ ID NO:44)	CAGCAGACTAAT AATGCTCCTGTT (SEQ ID NO:45)
MSPRO54	AATATGGCTTATACTAATTATCAGTATGTT AATATGCCTCATTTTGATTAT (SEQ ID NO:46)	CAGAGCTATGAC TATTTTAAGCTT (SEQ ID NO:47)
MSPRO55	TCTATGAATTCTACTATGTATTGGTATCTT CGTCGTGTTCTTTTTGAT CAT (SEQ ID NO:48)	CAGAGCTATGAC ATGTATAATTAT ATT (SEQ ID NO:49)
MSPRO59	TCTTATTAT CCTGATTTT GATTAT (SEQ ID NO:50)	CAGAGCTATGAC GGTCCTGATCTT TGG (SEQ ID NO:51)

Figure 30 provides the polynucleotide sequences of the preferred embodiments of the invention. The amino acid sequence of the VH and VL domains of the currently preferred embodiments of the present invention are presented below.

MS-Pro-2-VL(SEQ ID NO:92)

```
        1       DIELTQPPSV SVAP GQTARI SCSGD ALGDK YASWYQ QKPG QAPVLVI YDD

       51       SDRPSGIPER FSGS NSGNTA TLTIS GTQAE DEADYY CQSY DYSADYV FGG

      101       GTKLTVLGQ
```

MS-Pro-11-VL(SEQ ID NO:93)
```
        1       DIALTQPASV SGSP GQSITI SCTGT SSDVG GYNYVS WYQQ HPGKAPK LMI

       51       YDVSNRPSGV SNRF SGSKSG NTASL TISGL QAEDEA DYYC QSHHFYE VFG

      101       GGTKLTVLGQ
```

MS-PRO-12-VL (SEQ ID NO:94)
```
        1       DIELTQPPSV SVAP GQTARI SCSGD ALGDK YASWYQ QKPG QAPVLVI YDD

       51       SDRPSGIPER FSGS NSGNTA TLTIS GTQAE DEADYY CQSY DFDFAVF GGG

      101       TKLTVLGQ
```

MS-Pro-21-VL(SEQ ID NO:95)
```
        1       DIVMTQSPDS LAVS LGERAT INCRS SQSVL YSSNNK NYLA WYQQKPG QPP

       51       KLLIYWASTR ESGVP DRFSG SGSGTD FTLT ISSLQAE DVA VYYCQQYD SI

      101       PYTFGQGTKV EIKR T
```

MS-Pro-24-VL(SEQ ID NO:96)
```
        1       DIVLTQSPAT LSLS PGERAT LSCRA SQSVS SSYLAW YQQK PGQAPRL LIY

       51       GASSRATGVP ARFS GSGSGT DFTLT ISSLE PEDFAT YYCQ QMSNYPD TFG

      101       QGTKVEIKRT
```

MS-Pro-26-VL (SEQ ID NO:97)
```
        1       DIALTQPASV SGSP GQSITI SCTGT SSDVG GYNYVS WYQQ HPGKAPK LMI

       51       YDVSNRPSGV SNRF SGSKSG NTASL TISGL QAEDEA DYYC QSYDNNS DVV

      101       FGGGTKLTVL GQ
```

MS-Pro-28-VL (SEQ ID NO:98)
```
        1       DIQMTQSPSS LSAS VGDRVT ITCRA SQGIS SYLAWY QQKP GKAPKLL IYA

       51       ASSLQSGVPS RFSG SGSGTD FTLTI SSLQP EDFAVY YCFQ YGSIPPT FGQ

      101       GTKVEIKRT
```

MS-Pro-29-VL (SEQ ID NO:99)
```
1       DIVLTQSPAT LSLS PGERAT LSCRA SQSVS SSYLAW YQQK PGQAPRL LIY

51      GASSRATGVP ARFS GSGSGT DFTLT ISSLE PEDFAT YYCQ QTNNAPV TFG

101     QGTKVEIKRT
```

MS-Pro-54-VL (SEQ ID NO:10 0)
```
1       DIELTQPPSV SVAP GQTARI SCSGD ALGDK YASWYQ QKPG QAPVLVI YDD

51      SDRPSGIPER FSGS NSGNTA TLTIS GTQAE DEADYY CQSY DYFKLVF GGG

101     TKLTVLGQ
```

MS-Pro-55-VL (SEQ ID NO:10 1)
```
1       DIALTQPASV SGSP GQSITI SCTGT SSDVG GYNYVS WYQQ HPGKAPK LMI

51      YDVSNRPSGV SNRF SGSKSG NTASL TISGL QAEDEA DYYC QSYDMYN YIV

101     FGGGTKLTVL GQ
```

MS-Pro-59-VL (SEQ ID NO:10 2)
```
1       DIELTQPPSV SVAP GQTARI SCSGD ALGDK YASWYQ QKPG QAPVLVI YDD

51      SDRPSGIPER FSGS NSGNTA TLTIS GTQAE DEADYY CQSY DGPDLWV FGG

101     GTKLTVLGQ
```

MS-Pro-2-VH (SEQ ID NO:103)
```
1       QVQLVQSGAE VKKP GASVKV SCKAS GYTFT SYYMHW VRQA PGQGLEW MGW

51      INPNSGGTNY AQKF QGRVTM TRDTS ISTAY MELSSLR SED TAVYYCAR DF

101     LGYEFDYWGQ GTLV TVSS
```

MS-Pro-11-VH (SEQ ID NO:10 4)
```
1       QVQLVQSGAE VKKP GASVKV SCKAS GYTFT SYYMHW VRQA PGQGLEW MGW

51      INPNSGGTNY AQKF QGRVTM TRDTS ISTAY MELSSL RSED TAVYYCARYY

101     GSSLYHYVFG GFID YWGQGT LVTVS S
```

MS-Pro-12-VH(SEQ ID NO:10 5)
```
1       QVQLKESGPA LVKP TQTLTL TCTFS GFSLS TSGVGV GWIR QPPGKAL EWL

51      ALIDWDDDKY YSTS LKTRLT ISKDT SKNQV VLTMTN MDPV DTATYYC ARY

101     HSWYEMGYYG STVG YMFDYW GQGTL VTVSS
```

MS-Pro-21-VH (SEQ ID NO:10 6)
```
1       QVQLVQSGAE VKKP GSSVKV SCKAS GGTFS SYAISW VRQA PGQGLEW MGG

51      IIPIFGTANY AQKF QGRVTI TADES TSTAY MELSSL RSED TAVYYCA RDN

101     WFKPFSDVWG QGTLVTVSS
```

```
       MS-Pro-24-VH (SEQ ID NO:107)
         1           QVQLVQSGAE VKKP GSSVKV SCKAS GGTFS SYAISW VRQA PGQGLEW MGG

5        51          IIP IFGTANY AQKFQ GRVTI TADEST STAY MELSSLR SED TAVYYCAR VN

         101         HWTYTFDYWG QGTL VTVSS

       MS-Pro-26-VH ( SEQ ID NO:108)
10       1           QVQLVQSGAE VKKP GASVKV SCKAS GYTFT SYYMHW VRQA PGQGLEW MGW

         51          INPNSGGTNY AQKF QGRVTM TRDTS ISTAY MELSSL RSED TAVYYCA RGY

         101         WYAYFTYINY GYFD NWGQGT LVTVS S
15
       MS-Pro-28-VH ( SEQ ID NO:109)
         1           QVQLVQSGAE VKKP GSSVKV SCKAS GGTFS SYAISW VRQA PGQGLEW MGG

         51          IIP IFGTANY AQKF QGRVTI TADES TSTAY MELSSL RSED TAVYYCA RGG
20
         101         GWVSHGYYYL FDLW GQGTLV TVSS

       MS-Pro-29-VH ( SEQ ID NO:110)
         1           QVQLVQSGAE VKKP GASVKV SCKAS GYTFT SYYMHW VRQA PGQGLEW MGW
25
         51          INPNSGGTNY AQKF QGRVTM TRDTS ISTAY MELSSL RSED TAVYYCA RTW

         101         QYSYFYYLDG GYYF DIWGQG TLVTV SS

30     MS-Pro-54-VH (SEQ ID NO:111)
         1           QVQLVQSGAE VKKP GASVKV SCKAS GYTFT SYYMHW VRQA PGQGLEW MGW

         51          INPNSGGTNY AQKF QGRVTM TRDTS ISTAY MELSSL RSED TAVYYCA RNM

35       101         AYTNYQYVNM PHFD YWGQGT LVTVS S

       MS-Pro-55-VH (SEQ ID NO:112)
         1           QVQLVQSGAE VKKP GASVKV SCKAS GYTFT SYYMHW VRQA PGQGLEW MGW

40       51          INPNSGGTNY AQKF QGRVTM TRDTS ISTAY MELSSL RSED TAVYYCA RSM

         101         NSTMYWYLRR VLFD HWGQGT LVTVS S

       MS-Pro-59-VH (SEQ ID NO:113)
45       1           QVQLQQSGPG LVKP SQTLSL TCAIS GDSVS SNSAAW NWIR QSPGRGL EWL

         51          GRTYYRSKWY NDYA VSVKSR ITINP DTSKN QFSLQL NSVT PEDTAVY YCA

         101         RSYYPDFDYW GQGT LVTVSS
50
```

In addition to sequencing of the clones, a series of biochemical assays were performed to determine affinity and specificity of the molecules to the respective receptors. Table 1C lists the affinity of the respective molecules to FGFR3 and FGFR1 as measures by Biacore and/or FACS. In a binding assay to FGFR3-expressing cells the IC_{50} of the molecules was

calculated (Example 6). Domain specificity was determined as described in Example 9. The ligand-independent inhibition of FGFR3 (neutralizing activity) was determined as described in Example 11. Finally, the molecules were synthesized in a number of different formats including Fab, miniantibody (Fab-dHLX), IgG1, IgG4, IgG3 and as single chain Fv (scFv).

Table 1C

Clone	Affinity to FGFR3 (BIAcore)	Affinity to FGFR3 (FACS)	Affinity to FGFR1	Koff (s^{-1})	IC50 FR3 (FGF9)	Domain Specificity	Ligand independent inhibition of FGFR3	Available formats
MSPRO59	1.5nM	<1nM	-	7.1x10e-4	19 nM	2	+	Fab, Fab-dHLX IgG1, IgG4, mIgG3, scFv
MSPRO2	37nM	43 nM	-	2x10e-2	360 nM	2	~	Fab(+/- tags), Fab-dHLX, IgG1, IgG4,
MSPRO12	14nM	6.5 nM	-	2.3x10e-3	58 nM	2	+	Fab (+/- tag), Fab-dHLX, IgG1, IgG4, scFv
MSPRO11	4	4 nM	108	4 x 10e-4	220 nM	3		Fab. Fab-dHLX
MSPRO21	9 nM		-	3.6x10e-3	50 nM	3c		Fab, IgG1, Fab-dHLX
MSPRO24	10 nM		-	5.4x10e-3	70 nM	3c		Fab, IgG1
MSPRO26	4 nM	1.4		5 x 10e-4	70 nM	3		Fab, Fab-dHLX
MSPRO28	9 nM	0.3 nM	160 nM	4 x10e-3	50 nM	3		Fab
MSPRO29	6 nM	<1nM	29 nM	1.4x10e-3	20nM	3c	-	Fab (+/- tag), IgG1, IgG4, Fab-dHLX, scFv
MSPRO54	3.7nM		2.5nM	2x10e-3	45nM	3c		Fab, IgG1
MSPRO55	2.9nM		-	7.4x10e-4	34nM	3c		Fab

BiaCore results for certain molecules

In Table 1D the numbers are the IC_{50}s of the dimeric dHLX format of certain binders

(molecule with antigen binding site) in the FDCP-FGFR3 proliferation assay performed with

FGF9. The numbers in parentheses are the IC_{50} of the monomeric Fabs in the same assay.

5   Table 1E presents the KD value for certain MSPRO molecules in miniantibody form, as

determined in a Biacore.

Table 1D

binder	IC_{50}
MSPRO2	61 nM (360)
MSPRO12	26 nM (58)
MSPRO21	20 nM (50)
MSPRO26	8 nM (70)

Table 1E

10   **K_D determination for certain molecules**

Clone	BIAcore K_D [nM]	Number of measurements
MS-Pro-2-dHLX-MH	4.3 (37)	1
MS-Pro-11-dHLX-MH	0.7 (4)	1
MS-Pro-12-dHLX-MH	1.2 (14)	1
MS-Pro-21-dHLX-MH	2.2 (4.1)	1
MS-Pro-24-dHLX-MH	2 (10)	1
MS-Pro-26-dHLX-MH	2 (4)	1
MS-Pro-28-dHLX-MH	1.6 (9)	1

The preferred, but non-limiting, embodiments of molecules according to the present

invention that block constitutive (ligand-independent) activation of FGFR3 are referred to

herein MSPRO2, MSPRO12 and MSPRO59 comprising VH-CDR3 and VL-CDR3 domains

having SEQ ID Nos: 8 and 9; 12 and 13; and 24 and 25, respectively. The preferred, but non-

15   limiting, embodiments of molecules according to the present invention that block ligand-

dependent activation of FGFR3 are referred to herein MSPRO11, MSPRO21, MSPRO24,

MSPRO26, MSPRO29, and MSPRO54 comprising VH-CDR3 and VL-CDR3 domains

having SEQ ID Nos: 10 and 11; 14 and 15; 16 and 17, 18 and 19; 21 and 22; 23 and 24, respectively. Preferably, an antibody or a molecule of the present invention has an affinity (K_D) for binding a soluble dimeric form of FGFR3 of less than about 50 nM, preferably less than about 30 nM and more preferably less than about 10 nM, as determined by the BIAcore

5   chip assay for affinity, by a FACS-Scatchard analysis or other methods known in the art.

While the specific discovery of an antibody/molecule that blocks constitutive activation was made with respect to FGFR3 using a soluble dimeric form of FGFR3 to screen a phage display antibody library, it is believed that for all, or almost all receptor protein tyrosine kinases, antibodies/molecules that block constitutive activation can be similarly obtained

10   using a soluble dimeric form of a corresponding extracellular domain of a receptor protein tyrosine kinase. Non-limiting examples of receptor protein tyrosine kinases disclosed in Blume-Jensen et al. (2001) include EGFR/ErbB1, ErbB2/HER2/Neu, ErbB/HER3, ErbB4/HER4, IGF-1R, PDGFR-α, PDGFR-β, CSF-1R, kit/SCFR, Flk2/FH3, Flk1/VEGFR1, Flk1/VEGFR2, Flt4/VEGFR3, FGFR1, FGFR2/K-SAM, FGFR3, FGFR4, TrkA, TrkC,

15   HGFR, RON, EphA2, EphB2, EphB4, Axl, TIE/TIE1, Tek/TIE2, Ret, ROSAlk,Ryk, DDR, LTK and MUSK.

Furthermore, antibodies/molecules that block ligand-dependent or ligand independent activation of heterodimer receptor protein tyrosine kinases are intended to be included in the scope of the invention. Heterodimerization is well documented for members of the EGFR

20   subfamily of receptor protein tyrosine kinases and others. Non-limiting examples include EGFR/PDGFRβ, Flt1/KDR and EGFR/ErbB2 heterodimers. EGFR and PDGFRβ heterodimers have been identified as a mechanism for PDGF signal transduction in rat vascular smooth muscle cells (Saito et al., 2001) and Flt-1/KDR heterodimers are required for vinculin assembly in focal adhesions in response to VEGF signaling (Sato et al., 2000).

25   The present invention is also directed to a molecule having the antigen-binding portion of an antibody which binds to a dimeric form of an extracellular portion of a receptor protein tyrosine kinase (RPTK), such as a FGFR, and blocks the ligand-independent (constitutive) activation and/or ligand-dependent activation of the RPTK.

<u>Antibodies</u>

30   Antibodies, or immunoglobulins, comprise two heavy chains linked together by disulfide bonds and two light chains, each light chain being linked to a respective heavy chain by disulfide bonds in a "Y" shaped configuration. Proteolytic digestion of an antibody yields Fv

(Fragment variable and Fc (fragment crystalline) domains. The antigen binding domains, Fab', include regions where the polypeptide sequence varies. The term F(ab')$_2$ represents two Fab' arms linked together by disulfide bonds. The central axis of the antibody is termed the Fc fragment. Each heavy chain has at one end a variable domain (VH) followed by a number

5   of constant domains (CH). Each light chain has a variable domain (VL) at one end and a constant domain (CL) at its other end, the light chain variable domain being aligned with the variable domain of the heavy chain and the light chain constant domain being aligned with the first constant domain of the heavy chain (CH1).

The variable domains of each pair of light and heavy chains form the antigen binding site.

10   The domains on the light and heavy chains have the same general structure and each domain comprises four framework regions, whose sequences are relatively conserved, joined by three hypervariable domains known as complementarity determining regions (CDR1-3). These domains contribute specificity and affinity of the antigen binding site.

The isotype of the heavy chain (gamma, alpha, delta, epsilon or mu) determines

15   immunoglobulin class (IgG, IgA, IgD, IgE or IgM, respectively). The light chain is either of two isotypes (kappa,κ or lambda,λ) found in all antibody classes.

It should be understood that when the terms "antibody" or "antibodies" are used, this is intended to include intact antibodies, such as polyclonal antibodies or monoclonal antibodies (mAbs), as well as proteolytic fragments thereof such as the Fab or F(ab')$_2$ fragments. Further

20   included within the scope of the invention are chimeric antibodies; human and humanized antibodies; recombinant and engineered antibodies, and fragments thereof. Furthermore, the DNA encoding the variable region of the antibody can be inserted into the DNA encoding other antibodies to produce chimeric antibodies (see, for example, US patent 4,816,567). Single chain antibodies fall within the scope of the present invention. Single chain antibodies

25   can be single chain composite polypeptides having antigen binding capabilities and comprising amino acid sequences homologous or analogous to the variable regions of an immunoglobulin light and heavy chain (linked VH-VL or single chain Fv (ScFv)). Both V_H and V_L may copy natural monoclonal antibody sequences or one or both of the chains may comprise a CDR-FR construct of the type described in US patent 5,091,513, the entire

30   contents of which are hereby incorporated herein by reference. The separate polypeptides analogous to the variable regions of the light and heavy chains are held together by a polypeptide linker. Methods of production of such single chain antibodies, particularly

- 23 -

where the DNA encoding the polypeptide structures of the V_H and V_L chains are known, may be accomplished in accordance with the methods described, for example, in US patents 4,946,778, 5,091,513 and 5,096,815, the entire contents of each of which are hereby incorporated herein by reference.

5   Additionally, CDR grafting may be performed to alter certain properties of the antibody molecule including affinity or specificity. A non-limiting example of CDR grafting is disclosed in US patent 5,225,539.

A "molecule having the antigen-binding portion of an antibody" as used herein is intended to include not only intact immunoglobulin molecules of any isotype and generated by any

10   animal cell line or microorganism, but also the antigen-binding reactive fraction thereof, including, but not limited to, the Fab fragment, the Fab' fragment, the $F(ab')_2$ fragment, the variable portion of the heavy and/or light chains thereof, Fab miniantibodies (see WO 93/15210, US patent application 08/256,790, WO 96/13583, US patent application 08/817,788, WO 96/37621, US patent application 08/999,554, the entire contents of which

15   are incorporated herein by reference) and chimeric or single-chain antibodies incorporating such reactive fraction, as well as any other type of molecule or cell in which such antibody reactive fraction has been physically inserted, such as a chimeric T-cell receptor or a T-cell having such a receptor, or molecules developed to deliver therapeutic moieties by means of a portion of the molecule containing such a reactive fraction. Such molecules may be provided

20   by any known technique, including, but not limited to, enzymatic cleavage, peptide synthesis or recombinant techniques.

The term "Fc" as used herein is meant as that portion of an immunoglobulin molecule (Fragment crystallizable) that mediates phagocytosis, triggers inflammation and targets Ig to particular tissues; the Fc portion is also important in complement activation.

25   In one embodiment of the invention, a chimera comprising a fusion of the extracellular domain of the RPTK and an immunoglobulin constant domain can be constructed useful for assaying for ligands for the receptor and for screening for antibodies and fragments thereof

The "extracellular domain" when used herein refers the polypeptide sequence of the RPTKs disclosed herein which are normally positioned to the outside of the cell. The extracellular

30   domain encompasses polypeptide sequences in which part of or all of the adjacent (C-terminal) hydrophobic transmembrane and intracellular sequences of the mature RPTK have

been deleted. Thus, the extracellular domain-containing polypeptide can comprise the extracellular domain and a part of the transmembrane domain. Alternatively, in the preferred embodiment, the polypeptide comprises only the extracellular domain of the RPTK. The truncated extracellular domain is generally soluble. The skilled practitioner can readily

5   determine the extracellular and transmembrane domains of a RPTK by aligning the RPTK of interest with known RPTK amino acid sequences for which these domains have been delineated. Alternatively, the hydrophobic transmembrane domain can be readily delineated based on a hydrophobicity plot of the polypeptide sequence. The extracellular domain is N-terminal to the transmembrane domain.

10 The term "epitope" is meant to refer to that portion of any molecule capable of being bound by an antibody or a fragment thereof which can also be recognized by that antibody. Epitopes or antigenic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and have specific three-dimensional structural characteristics as well as specific charge characteristics.

15 An "antigen" is a molecule or a portion of a molecule capable of being bound by an antibody which is additionally capable of inducing an animal to produce antibody capable of binding to an epitope of that antigen. An antigen may have one or more than one epitope. The specific reaction referred to above is meant to indicate that the antigen will react, in a highly selective manner, with its corresponding antibody and not with the multitude of other

20 antibodies which may be evoked by other antigens.

A "neutralizing antibody" as used herein refers to a molecule having an antigen binding site to a specific receptor capable of reducing or inhibiting (blocking) activity or signaling through a receptor, as determined by *in vivo* or *in vitro* assays, as per the specification.

A monoclonal antibody (mAb) is a substantially homogeneous population of antibodies to a

25 specific antigen. MAbs may be obtained by methods known to those skilled in the art. See, for example Kohler et al (1975); US patent 4,376,110; Ausubel et al (1987-1999); Harlow et al (1988); and Colligan et al (1993), the contents of which references are incorporated entirely herein by reference. The mAbs of the present invention may be of any immunoglobulin class including IgG, IgM, IgE, IgA, and any subclass thereof. A hybridoma

30 producing an mAb may be cultivated *in vitro* or *in vivo*. High titers of mAbs can be obtained in *in vivo* production where cells from the individual hybridomas are injected intraperitoneally into pristine-primed Balb/c mice to produce ascites fluid containing high

concentrations of the desired mAbs. MAbs of isotype IgM or IgG may be purified from such ascites fluids, or from culture supernatants, using column chromatography methods well known to those of skill in the art.

Chimeric antibodies are molecules, the different portions of which are derived from different
5   animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. Antibodies which have variable region framework residues substantially from human antibody (termed an acceptor antibody) and complementarity determining regions substantially from a mouse antibody (termed a donor antibody) are also referred to as humanized antibodies. Chimeric antibodies are primarily
10 used to reduce immunogenicity in application and to increase yields in production, for example, where murine mAbs have higher yields from hybridomas but higher immunogenicity in humans, such that human/murine chimeric mAbs are used. Chimeric antibodies and methods for their production are known in the art (Better et al, 1988; Cabilly et al, 1984; Harlow et al, 1988; Liu et al, 1987; Morrison et al, 1984; Boulianne et al, 1984;
15 Neuberger et al, 1985; Sahagan et al , 1986; Sun et al, 1987; Cabilly et al; European Patent Applications 125023, 171496, 173494, 184187, 173494, PCT patent applications WO 86/01533, WO 97/02671, WO 90/07861, WO 92/22653 and US patents 5,693,762, 5,693,761, 5,585,089, 5,530,101 and 5,225,539). These references are hereby incorporated by reference.

20 Besides the conventional method of raising antibodies *in vivo*, antibodies can be generated *in vitro* using phage display technology. Such a production of recombinant antibodies is much faster compared to conventional antibody production and they can be generated against an enormous number of antigens. In contrast, in the conventional method, many antigens prove to be non-immunogenic or extremely toxic, and therefore cannot be used to generate
25 antibodies in animals. Moreover, affinity maturation (i.e., increasing the affinity and specificity) of recombinant antibodies is very simple and relatively fast. Finally, large numbers of different antibodies against a specific antigen can be generated in one selection procedure. To generate recombinant monoclonal antibodies one can use various methods all based on phage display libraries to generate a large pool of antibodies with different antigen
30 recognition sites. Such a library can be made in several ways: One can generate a synthetic repertoire by cloning synthetic CDR3 regions in a pool of heavy chain germline genes and thus generating a large antibody repertoire, from which recombinant antibody fragments with

various specificities can be selected. One can use the lymphocyte pool of humans as starting material for the construction of an antibody library. It is possible to construct naive repertoires of human IgM antibodies and thus create a human library of large diversity. This method has been widely used successfully to select a large number of antibodies against

5   different antigens. Protocols for bacteriophage library construction and selection of recombinant antibodies are provided in the well-known reference text Current Protocols in Immunology, Colligan et al (Eds.), John Wiley & Sons, Inc. (1992-2000), Chapter 17, Section 17.1.

Another aspect of the present invention is directed to a method for screening for the antibody

10 or molecule of the present invention by screening a library of antibody fragments displayed on the surface of bacteriophage, such as disclosed in the Example herein and described in WO 97/08320, US Patent 6,300,064 , and Knappik et al. (2000), for binding to a soluble dimeric form of a receptor protein tyrosine kinase. An antibody fragment which binds to the soluble dimeric form of the RPTK used for screening is identified as a candidate molecule for

15 blocking ligand-dependent activation and/or constitutive activation of the RPTK in a cell. Preferably the RPTK of which a soluble dimeric form is used in the screening method is a fibroblast growth factor receptor (FGFR), and most preferably FGFR3.

As a first screening method, the soluble dimeric form of a receptor tyrosine kinase can be constructed and prepared in a number of different ways. For instance, the extracellular

20 domain of a RPTK joined to Fc and expressed as a fusion polypeptide that dimerizes naturally by means of the Fc portion of the RPTK-Fc fusion. Other suitable types of constructs of FGFR3, serving as guidance for other RPTKs, are disclosed in the Examples presented herein.

The assays for determining binding of antibody fragments to FGFR3, binding affinities,

25 inhibition of cell proliferation, etc., are also described in the Examples herein below.

The term "cell proliferation" refers to the rate at which a group of cells divides. The number of cells growing in a vessel can be quantified by a person skilled in the art when that person visually counts the number of cells in a defined volume using a common light microscope. Alternatively, cell proliferation rates can be quantified by laboratory apparati that optically or

30 conductively measure the density of cells in an appropriate medium.

A second screen for antibody fragments as candidate molecules can be done using cells having very high over expression of the RPTK, such as for instance RCJ-M15 cells

overexpressing mutant (achondroplasia) FGFR3. In cells expressing very high levels of receptor some ligand-independent activation occurs even without the presence of a mutation, such as a constitutive activation mutation. It is believed that RPTK overexpression forces RPTKs to dimerize and signal even in the absence of ligand. These cells have monomeric receptors as well as dimeric receptors present on their cell surface. Using this type of cell, one of skill in the art would be able to identify all different kinds of antibodies, i.e., blocking ligand-dependent activation, blocking constitutive activation, blocking activation and binding only to monomeric form, etc.

A third screen can be carried out on a cell line expressing a RPTK carrying a mutation, such as the FDCP-FR3ach line expressing the FGFR3 achondroplasia mutation. The receptors of this line become constitutively active, e.g. are able to signal in the absence of a ligand as determined by ERK (MAPK) phosphorylation, a downstream effector.

A further aspect of the present invention relates to a method for treating or inhibiting a skeletal dysplasia or craniosynostosis disorder associated with constitutive activation of a RPTK which involves administering the molecule of the present invention to a subject need thereof. Non-limiting examples of skeletal dysplasias include achondroplasia, thanatophoric dysplasia (TDI or TDII), hypochondroplasia, and severe achondroplasia with developmental delay and acanthosis nigricans (SADDAN) dysplasia. Non-limiting examples of craniosynostosis disorder are Muenke coronal craniosynostosis and Crouzon syndrome with acanthosis nigricans. The symptoms and etiology of these diseases and disorders are reviewed in Vajo et al. (Vajo et al, 2000).

The present invention also provides for a method for treating or inhibiting a cell proliferative disease or disorder associated with the action of an abnormal constitutively activated RPTK, for example. tumor formation, primary tumors, tumor progression or tumor metastasis. A molecule containing the antigen binding portion of an antibody that blocks constitutive activation of a RPTK is administered to a subject in need thereof to treat or inhibit such a cell proliferative disease or disorder.

The terms "treating or inhibiting a proliferative disease or disorder" or "treating or inhibiting a tumor" are used herein and in the claims to encompass tumor formation, primary tumors, tumor progression or tumor metastasis.

Tumor formation or tumor growth are intended to encompass solid and non-solid tumors. Solid tumors include mammary, ovarian, prostate, colon, cervical, gastric, esophageal,

papillary thyroid, pancreatic, bladder, colorectal, melanoma, small-cell lung and non-small-cell lung cancers, granulose cell carcinoma, transitional cell carcinoma, vascular tumors, all types of sarcomas, e.g. osteosarcoma, chondrosarcoma, Kaposi's sarcoma, myosarcoma, hemangiosarcoma, and glioblastomas.

5   Non-solid tumors include for example hematopoietic malignancies such as all types of leukemia, e.g. chronic myelogenous leukemia (CML), acute myelogenous leukemia (AML), mast cell leukemia, chronic lymphocytic leukemia (CLL) and acute lymphocytic leukemia (ALL), lymphomas, and multiple myeloma (MM).

Tumor progression is the phenomenon whereby cancers become more aggressive with time.
10   Progression can occur in the course of continuous growth, or when a tumor recurs after treatment and includes progression of transitional cell carcinoma, osteo or chondrosarcoma, multiple myeloma, and mammary carcinoma (one of the known RPTKs involved in mammary carcinoma is ErbB3).

The role of the FGFR3 in tumor progression associated with transitional cell carcinoma and
15   multiple myeloma has recently been elucidated (Cappellen, et al, 1999; Chesi, et al, 2001)

In another aspect of the present invention, molecules which bind FGFR, more preferably FGFR3, and block ligand-dependent receptor activation are provided. These molecules are useful in treating hyperproliferative diseases or disorders and non-neoplastic angiogenic pathologic conditions such as neovascular glaucoma, proliferative retinopathy including
20   proliferative diabetic retinopathy, macular degeneration, hemangiomas, angiofibromas, and psoriasis. The role of FGFs and their receptors in neo- and hypervascularization has been well documented (Frank, 1997; Gerwins et al, 2000)

In another aspect of the present invention, the pharmaceutical compositions according to the present invention is similar to those used for passive immunization of humans with other
25   antibodies. Typically, the molecules of the present invention comprising the antigen binding portion of an antibody will be suspended in a sterile saline solution for therapeutic uses. The pharmaceutical compositions may alternatively be formulated to control release of active ingredient (molecule comprising the antigen binding portion of an antibody) or to prolong its presence in a patient's system. Numerous suitable drug delivery systems are known and
30   include, e.g., implantable drug release systems, hydrogels, hydroxymethylcellulose, microcapsules, liposomes, microemulsions, microspheres, and the like. Controlled release preparations can be prepared through the use of polymers to complex or adsorb the molecule

according to the present invention. For example, biocompatible polymers include matrices of poly(ethylene-co-vinyl acetate) and matrices of a polyanhydride copolymer of a stearic acid dimer and sebaric acid (Sherwood et al, 1992). The rate of release molecule according to the present invention, i.e., of an antibody or antibody fragment, from such a matrix depends upon the molecular weight of the molecule, the amount of the molecule within the matrix, and the size of dispersed particles (Saltzman et al., 1989 and Sherwood et al., 1992). Other solid dosage forms are described in (Ansel et al., 1990 and Gennaro, 1990).

The pharmaceutical composition of this invention may be administered by any suitable means, such as orally, intranasally, subcutaneously, intramuscularly, intravenously, intra-arterially, intralesionally or parenterally. Ordinarily, intravenous (i.v.) or parenteral administration will be preferred.

It will be apparent to those of ordinary skill in the art that the therapeutically effective amount of the molecule according to the present invention will depend, *inter alia* upon the administration schedule, the unit dose of molecule administered, whether the molecule is administered in combination with other therapeutic agents, the immune status and health of the patient, the therapeutic activity of the molecule administered and the judgment of the treating physician. As used herein, a "therapeutically effective amount" refers to the amount of a molecule required to alleviate one or more symptoms associated with a disorder being treated over a period of time.

Although an appropriate dosage of a molecule of the invention varies depending on the administration route, age, body weight, sex, or conditions of the patient, and should be determined by the physician in the end, in the case of oral administration, the daily dosage can generally be between about 0.01-200 mg, preferably about 0.01-10 mg, more preferably about 0.1-10 mg, per kg body weight. In the case of parenteral administration, the daily dosage can generally be between about 0.001-100 mg, preferably about 0.001-1 mg, more preferably about 0.01-1 mg, per kg body weight. The daily dosage can be administered, for example in regimens typical of 1-4 individual administration daily. Various considerations in arriving at an effective amount are described, e.g., in Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th ed., Pergamon Press, 1990; and Remington's Pharmaceutical Sciences, 17th ed., Mack Publishing Co., Easton, Pa., 1990.

The molecule of the present invention as an active ingredient is dissolved, dispersed or admixed in an excipient that is pharmaceutically acceptable and compatible with the active

ingredient as is well known. Suitable excipients are, for example, water, saline, phosphate buffered saline (PBS), dextrose, glycerol, ethanol, or the like and combinations thereof. Other suitable carriers are well-known to those in the art. (See, for example, Ansel et al., 1990 and Gennaro, 1990). In addition, if desired, the composition can contain minor

5   amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents.

Combination therapy

The combined treatment of one or more of the molecules of the invention with an anti-neoplastic or anti-chemotherapeutic drug such as doxorubicin, cisplatin or taxol provides a more efficient treatment for inhibiting the growth of tumor cells than the use of the molecule

10   by itself. In one embodiment, the pharmaceutical composition comprises the antibody and carrier with an anti-chemotherapeutic drug.

The present invention also provides for a nucleic acid molecule, which contains a nucleotide sequence encoding the molecule having the antigen binding portion of an antibody that blocks ligand-dependent activation and/or constitutive activation of a receptor protein

15   tyrosine kinase such as FGFR3, and a host cell transformed with this nucleic acid molecule. Furthermore, also within the scope of the present invention is a nucleic acid molecule containing a nucleotide sequence having at least 90% sequence identity, preferably about 95%, and more preferably about 97% identity to the above encoding nucleotide sequence as would well understood by those of skill in the art.

20   The invention also provides nucleic acids that hybridize under high stringency conditions to polynucleotides having SEQ ID NOs: 8 through 29 and SEQ ID NOs: 62, 64-65, 67, 69-71, 73-76 78-80, 82-87, 89, 90-91 or the complement thereof. As used herein, highly stringent conditions are those which are tolerant of up to about 5-20% sequence divergence, preferably about 5-10%. Without limitation, examples of highly stringent (-10°C below the calculated

25   Tm of the hybrid) conditions use a wash solution of 0.1 X SSC (standard saline citrate) and 0.5% SDS at the appropriate Ti below the calculated Tm of the hybrid. The ultimate stringency of the conditions is primarily due to the washing conditions, particularly if the hybridization conditions used are those which allow less stable hybrids to form along with stable hybrids. The wash conditions at higher stringency then remove the less stable hybrids.

30   A common hybridization condition that can be used with the highly stringent to moderately stringent wash conditions described above is hybridization in a solution of 6 X SSC (or 6 X SSPE), 5 X Denhardt's reagent, 0.5% SDS, 100 µg/ml denatured, fragmented salmon sperm

DNA at an appropriate incubation temperature Ti. *See generally* Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2d edition, Cold Spring Harbor Press (1989)) for suitable high stringency conditions.

Stringency conditions are a function of the temperature used in the hybridization experiment and washes, the molarity of the monovalent cations in the hybridization solution and in the wash solution(s) and the percentage of formamide in the hybridization solution. In general, sensitivity by hybridization with a probe is affected by the amount and specific activity of the probe, the amount of the target nucleic acid, the detectability of the label, the rate of hybridization, and the duration of the hybridization. The hybridization rate is maximized at a Ti (incubation temperature) of 20-25°C below Tm for DNA:DNA hybrids and 10-15°C below Tm for DNA:RNA hybrids. It is also maximized by an ionic strength of about 1.5M Na^+. The rate is directly proportional to duplex length and inversely proportional to the degree of mismatching.

Specificity in hybridization, however, is a function of the difference in stability between the desired hybrid and "background" hybrids. Hybrid stability is a function of duplex length, base composition, ionic strength, mismatching, and destabilizing agents (if any).

The Tm of a perfect hybrid may be estimated for DNA:DNA hybrids using the equation of Meinkoth et al (1984), as

$$Tm = 81.5°C + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$$

and for DNA:RNA hybrids, as

$$Tm = 79.8°C + 18.5 (\log M) + 0.58 (\%GC) - 11.8 (\%GC)^2 - 0.56(\% \text{ form}) - 820/L$$

where   M, molarity of monovalent cations, 0.01-0.4 M NaCl,

                   %GC, percentage of G and C nucleotides in DNA, 30%-75%,

                   % form, percentage formamide in hybridization solution, and

                   L, length hybrid in base pairs.

Tm is reduced by 0.5-1.5°C (an average of 1°C can be used for ease of calculation) for each 1% mismatching.

The Tm may also be determined experimentally. As increasing length of the hybrid (L) in the above equations increases the Tm and enhances stability, the full-length rat gene sequence can be used as the probe.

Filter hybridization is typically carried out at 68°C, and at high ionic strength (e.g., 5 - 6 X
SSC), which is non-stringent, and followed by one or more washes of increasing stringency,
the last one being of the ultimately desired high stringency. The equations for Tm can be
used to estimate the appropriate Ti for the final wash, or the Tm of the perfect duplex can be

5   determined experimentally and Ti then adjusted accordingly.

The present invention also relates to a vector comprising the nucleic acid molecule of the
present invention. The vector of the present invention may be, e.g., a plasmid, cosmid, virus,
bacteriophage or another vector used e.g. conventionally in genetic engineering, and may
comprise further genes such as marker genes which allow for the selection of said vector in a

10   suitable host cell and under suitable conditions.

Furthermore, the vector of the present invention may, in addition to the nucleic acid
sequences of the invention, comprise expression control elements, allowing proper
expression of the coding regions in suitable hosts. Such control elements are known to the
artisan and may include a promoter, a splice cassette, translation initiation codon, translation

15   and insertion site for introducing an insert into the vector.

Preferably, the nucleic acid molecule of the invention is operatively linked to said expression
control sequences allowing expression in eukaryotic or prokaryotic cells.

Control elements ensuring expression in eukaryotic or prokaryotic cells are well known to
those skilled in the art. As mentioned herein above, they usually comprise regulatory

20   sequences ensuring initiation of transcription and optionally poly-A signals ensuring
termination of transcription and stabilization of the transcript.

Methods for construction of nucleic acid molecules according to the present invention, for
construction of vectors comprising said nucleic acid molecules, for introduction of said
vectors into appropriately chosen host cells, for causing or achieving the expression are well-

25   known in the art (see, e.g., Sambrook et al., 1989; Ausubel et al., 1994).

The invention also provides for conservative amino acid variants of the molecules of the
invention. Variants according to the invention also may be made that conserve the overall
molecular structure of the encoded proteins. Given the properties of the individual amino
acids comprising the disclosed protein products, some rational substitutions will be

30   recognized by the skilled worker. Amino acid substitutions, *i.e.* "conservative substitutions,"
may be made, for instance, on the basis of similarity in polarity, charge, solubility,
hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved.

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For example: (a) nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (b) polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; (c) positively charged (basic) amino acids include arginine, lysine, and histidine; and (d)

5   negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Substitutions typically may be made within groups (a)-(d). In addition, glycine and proline may be substituted for one another based on their ability to disrupt α-helices. Similarly, certain amino acids, such as alanine, cysteine, leucine, methionine, glutamic acid, glutamine, histidine and lysine are more commonly found in α helices, while valine, isoleucine,

10   phenylalanine, tyrosine, tryptophan and threonine are more commonly found in β-pleated sheets. Glycine, serine, aspartic acid, asparagine, and proline are commonly found in turns. Some preferred substitutions may be made among the following groups: (i) S and T; (ii) P and G; and (iii) A, V, L and 1. Given the known genetic code, and recombinant and synthetic DNA techniques, the skilled scientist readily can construct DNAs encoding the conservative

15   amino acid variants.

As used herein, "sequence identity" between two polypeptide sequences indicates the percentage of amino acids that are identical between the sequences. "Sequence similarity" indicates the percentage of amino acids that either are identical or that represent conservative amino acid substitutions.

20   <u>Conjugates</u>

One embodiment of the present invention provides molecules of the present invention conjugated to cytotoxins. The cytotoxic moiety of the antibody may be a cytotoxic drug or an enzymatically active toxin or bacterial or plant origin, or an enzymatically active fragment of such a toxin including, but not limited to, diphtheria A chain, nonbinding active fragments of

25   diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, curcin, crotin, saponin, gelonin, mitogellin, restrictocin, phenomycin, and enomycin. In another embodiment, the molecules of the present invention are conjugate to small molecule anti-cancer drugs. Conjugates of the antibody and such cytotoxic moieties are made using a

30   variety of bifunctional protein coupling agents. Examples of such reagents include SPDP, IT, bifunctional derivatives of imidoesters such a dimethyl adipimidate HCl, active esters such as disuccinimidyl suberate, aldehydes such as glutaraldehyde, bis-azido compounds such as bis-

(p-azidobenzoyl) hexanediamine, bis-diazonium derivatives, dissocyanates and bis-active fluorine compounds. The lysing portion of a toxin may be joined to the Fab fragment of the antibodies.

Additionally, the molecules of the present invention can also be detected *in vivo* by imaging, for example imaging of cells which have undergone tumor progression or have metastasized. Antibody labels or markers for *in vivo* imaging of RPTKs include those detectable by X-radiography, NMR, PET, or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody.

A specific antibody or antibody portion which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I, ^{111}In, ^{99}Tc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously or intraperitoneally) into the mammal to be examined for a disorder. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moieties needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries. The labeled antibody or antibody portion will then preferentially accumulate at the location of cells which contain a specific RPTK. In vivo tumor imaging is described in Burchiel et al., (1982

The methods and compositions described herein may be performed, for example, by utilizing pre-packaged diagnostic test kits comprising in one or more containers (i) at least one immunoglobulin of the invention and (ii) a reagent suitable for detecting the presence of said immunoglobulin when bound to its target. A kit may be conveniently used, e.g., in clinical settings or in home settings, to diagnose patients exhibiting a disease (e.g., skeletal dysplasia, craniosynostosis disorders, cell proliferative diseases or disorders, or tumor progression), and to screen and identify those individuals exhibiting a predisposition to such disorders. A composition of the invention also may be used in conjunction with a reagent suitable for detecting the presence of said immunoglobulin when bound to its target, as well as instructions for use, to carry out one or more methods of the invention.

Having now generally described the invention, the same will be more readily understood through reference to the following examples, which are provided by way of illustration and are not intended to be limiting of the present invention.

EXAMPLES

5   An important approach to control FGFR3 activity is the generation of reagents that block receptor signaling. Without wishing to be bound by theory, molecules which bind the extracellular domain of the receptor may inhibit the receptor by competing with FGF or heparin binding or, alternatively, by preventing receptor dimerization. Additionally, binding to the extracellular domain may accelerate receptor internalization and turnover. Humanized

10   antibodies are expected to have inhibitory/neutralizing action and are of particular interest since they are considered to be valuable for therapeutic applications, avoiding the human anti-mouse antibody response frequently observed with rodent antibodies. The experiments in which the neutralizing antibodies are screened, identified and obtained using fully synthetic human antibody libraries (for discovering highly specific binders against a wide

15   variety of antigens) and FGFR3 extracellular domain are described below.

Example 1: Attempt to generate anti-FGFR3 antibodies

One hundred micrograms of soluble FGFR3 in complete Freund's Adjuvant were injected into Balb/c 3T3 naive mice (9 animals). Two repeated injections of 20 micrograms were

20   performed at week intervals. 10 days after the second booster injection, blood was drawn from animals and serum was tested for the presence of polyclonal antibodies both by monitoring for binding to the receptor as well as for neutralizing activity at a dilution of 1:50. No significant neutralizing activity was observed in the tested serum (20% at most in some animals). A prefusion injection of 20 micrograms of soluble receptor was administered 1-2

25   days later but all the mice harboring some activity of neutralizing Ab died. The experiment was repeated twice with the same results.

Example 2: Generation of the FGFR3 Antigens

Two dimeric forms of the extracellular domain of the human FGFR3 were prepared for use as antigen. One was a histidine-tagged domain with a Serine 371 to Cysteine (S371C)

30   substitution (thanatophoric dysplasia (TD) mutation) to facilitate dimerization and the second one an Fc fusion. The S371C variant was shown to bind heparin and FGF9 coated plates and

to inhibit FGF9-dependent FDCP-FR3 proliferation. The Fc fusion was similarly effective in binding assays demonstrating its potential as an inhibitor of FGFR function and as a target for selecting FGFR3 inhibitory molecules. Both soluble receptors were employed to select neutralizing human recombinant antibodies.

5   The two variants of the FGFR3 extracellular domain were prepared as follows:

1. A construct containing the extracellular portion of FGFR3 with a thanatophoric dysplasia (TD) mutation to facilitate dimer formation conjugated to a His-tag (histidine tag) was generated. A bluescript plasmid comprising the human FGFR3 gene (pBS-hFGFR3) was used as template for PCR with the following primers:

10   5'-ACGTGCTAGC TGAGTCCTTG GGGACGGAGC AG   (SEQ ID NO:2).

5'-ACGTCTCGAG TTAATGGTGA TGGTGATGGT GTGCATACAC **ACA**GCCCGCC TCGTC (SEQ ID NO:3),

wherein the Ser 371 Cys (S371C) substitution is bold and underlined.

The nucleotide sequence encoding the extracellular domain of FGFR3 with the TD

15   substitution is denoted herein SEQ ID NO:7:

```
     TGAGTCCTTG GGG ACGGAGC AGCG CGTCGT GGGGC GAGCG GCAGAA GTCC CGGGCCC AGA   60
     GCCCGGCCAG CAG GAGCAGT TGG TCTTCGG CAGC GGGGAT GCTGT GGAGC TGAGCT GTCC  120
     CCCGCCCGGG GGT GGTCCCA TGGG GCCCAC TGTCT GGGTC AAGGAT GGCA CAGGGCT GGT  180
     GCCCTCGGAG CGT GTCCTGG TGGG GCCCCA GCGGC TGCAG GTGCTG AATG CCTCCCA CGA  240
     GGACTCCGGG GCC TACAGCT GCCG GCAGCG GCTCA CGCAG CGCGTA CTGT GCCACTT CAG  300
     TGTGCGGGTG ACA GACGCTC CATC CTCGGG AGATG ACGAA GACGGG GAGG ACGAGGC TGA  360
     GGACACAGGT GTG GACACAG GGGC CCCTTA CTGGA CACGG CCCGAG CGGA TGGACAA GAA  420
     GCTGCTGGCC GTG CCGGCCG CCAA CACCGT CCGCT TCCGC TGCCCA GCCG CTGGCAA CCC  480
     CACTCCCTCC ATC TCCTGGC TGAA GAACGG CAGGG AGTTC CGCGGC GAGC ACCGCAT TGG  540
     AGGCATCAAG CTG CGGCATC AGCA GTGGAG CCTGG TCATG GAAAGC GTGG TGCCCTC GGA  600
     CCGCGGCAAC TAC ACCTGCG TCGT GGAGAA CAAGT TTGGC AGCATC CGGC AGACGTA CAC  660
     GCTGGACGTG CTG GAGCGCT CCCC GCACCG GCCCA TCCTG CAGGCG GGGC TGCCGGC CAA  720
     CCAGACGGCG GTG CTGGGCA GCGA CGTGGA GTTCC ACTGC AAGGTG TACA GTGACGC ACA  780
     GCCCCACATC CAG TGGCTCA AGCA CGTGGA GGTGA ACGGC AGCAAG GTGG GCCCGGA CGG  840
     CACACCCTAC GTT ACCGTGC TCAA GACGGC GGGCG CTAAC ACCACC GACA AGGAGCT AGA  900
     GGTTCTCTCC TTG CACAACG TCAC CTTTGA GGACG CCGGG GAGTAC ACCT GCCTGG CGGG  960
     CAATTCTATT GGG TTTTCTC ATCA CTCTGC GTGGC TGGTG GTGCTG CCAG CCGAGGA GGA 1020
     GCTGGTGGAG GCT GACGAGG CGGG CTGTGT GTATG CACAC CATCAC CATC ACCATTA A     1078
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The PCR fragment was digested with XhoI and ligated into pBlueScript digested with

35   EcoRV and XhoI. The resulting plasmid, pBsFR3[23-374]Tdhis, was cleaved with NdeI and

XhoI and the DNA fragment encoding the extracellular domain of FGFR3 was ligated into the same restriction sites in pCEP-Pu/Ac7 (Yamaguchi et al., 1999; Kohfeldt et al., 1997), generating the pCEP-hFR3$^{23-374}$TDhis plasmid construct.

To express this FGFR3 variant, 293E cells (EBNA virus transfected 293 cells) were

5   transfected with the aforementioned plasmid, pCEP-hFR3$^{23-374}$TDhis, clones were identified and grown. Cell supernatants analyzed by Western blot with anti-His antibody demonstrated high expression of the soluble receptor. Supernatants from large scale preparations were then subjected to batch affinity purification with Ni-NTA beads and the tagged soluble receptor was eluted by a step gradient ranging from 20 mM to 500 mM imidazol. A sample from each

10   eluate was loaded onto a 7.5% SDS-PAGE and stained with GelCode (Pierce). In parallel Western blot analysis was performed and analyzed with anti-His antibodies. SDS-PAGE (Fig. 1) and immunoblot (not shown) analyses demonstrated peak amounts of purified extracellular FGFR3 in the 2nd (2) 50 mM imidazol fraction. About 0.5 mg of pure protein was obtained following this single step purification. In Figure 1, T=total protein, D= dialysed

15   protein, U= unbound fraction.

To assess whether hFR3$^{23-374}$TDhis (hFR3-TDhis) retained the ability to associate with heparin and heparin-FGF complex, heparin coated wells were incubated with purified (2, 4 or 10 µg, labeled as FR3 2, FR3 4 or FR3 10, respectively in Fig. 2) or unpurified (FR3 sup) hFR3$^{23-374}$TDhis with (checkered bar) or without FGF9 (200ng/well, hatched bar). The

20   binding of hFR3$^{23-374}$TDhis to each well was determined with anti-His antibody. Mock supernatant (M sup), PBS and unpurified mouse FR3AP (FGFR3-alkaline phosphatase, labeled as FRAP sup) were included as controls. This demonstrated that, like what was reported for the wild-type receptor, hFR3$^{23-374}$TDhis binds to heparin and that this interaction is augmented by the presence of FGF9 (Fig. 2). Finally, it was demonstrated that hFR3^{23-}

25   ^{374}TDhis inhibits FDCP-FR3 FGF-dependent proliferation in a dose dependent manner. hFR3$^{23-374}$TDhis had no inhibitory effect on proliferation when FDCP-FR3 cells were grown in the presence of IL-3. Taken together, hFR3$^{23-374}$TDhis proved to be a good candidate as a target antigen for screening for FGFR3 neutralizing antibodies.

2. The extracellular domain of FGFR3 and FGFR1 were prepared as Fc fusions (FR3exFc

30   and FR1exFc). The amino acid sequence of FGFR3 (NCBI access no: NP_000133) is denoted herein SEQ ID NO:1.

1 MGA PACALAL CVAV AIVAGA SSESL GTEQR VVGRAA EVPG PEPGQQE QLV FGSGDAVE LS

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 61  CPPP GGGPMG  PTVWV KDGTG  LVPSER VLVG  PQRLQVL NAS  HEDSGAYS CR  QRLTQRVLC H
121  FSV RVTDAPS  SGDD EDGEDE  AEDTG VDTGA  PYWTRP ERMD  KKLLAVP AAN  TVRFRCPA AG
181  NPTP SISWLK  NGREF RGEHR  IGGIKL RHQQ  WSLVMES VVP  SDRGNYTC VV  ENKFGSIRQ T
241  YTLD VLERSP  HRPIL QAGLP  ANQTAV LGSD  VEFHCKV YSD  AQPHIQWL KH  VEVNGSKVG P
301  DGTP YVTVLK  TAGAN TTDKE  LEVLS LHNVT  FEDAGE YTCL  AGNSIGF SHH  SAWLVVLP AE
361  EELV EADEAG  SVYAG ILSYG  VGFFLF ILVV  AAVTLCR LRS  PPKKGLGS PT  VHKISRFPL K
421  RQVS LESNAS  MSSNT PLVRI  ARLSSG EGPT  LANVSEL ELP  ADPKWELS RA  RLTLGKPLG E
481  GCFG QVVMAE  AIGID KDRAA  KPVTVA VKML  KDDATDK DLS  DLVSEMEM MK  MIGKHKNII N
541  LLGA CTQGGP  LYVLV EYAAK  GNLREF LRAR  RPPGLDY SFD  TCKPPEEQ LT  FKDLVSCAY Q
601  VARG MEYLAS  QKCIH RDLAA  RNVLVT EDNV  MKIADFG LAR  DVHNLDYY KK  TTNGRLPVK W
661  MAPE ALFDRV  YTHQS DVWSF  GVLLWE IFTL  GGSPYPG IPV  EELFKLLK EG  HRMDKPANC T
721  HDLY MIMREC  WHAAP SQRPT  FKQLVE DLDR  VLTVTST DEY  LDLSAPFE QY  SPGGQDTPS S
781  SSSG DDSVFA  HDLLP PAPPS  SGGSRT
```

To construct the FR3exFc fusion, a nucleotide sequence (SEQ ID NO:4) encoding the extracellular domain of FGFR3 was PCR amplified to contain terminal KpnI and BamHI restriction sites for insertion into the KpnI and BamHI sites of pCXFc (SEQ ID NO:5). This insertion positions the extracellular domain of FGFR3 to be expressed as a fusion with the Fc amino acid sequence (SEQ ID NO:6).

SEQ ID NO:4:

```
GCGCGCTGCC TGAGGACGCC GCGG CCCCCG CCCCC GCCAT GGGCGC CCCT GCCTGCG CCC      60
TCGCGCTCTG CGT GGCCGTG GCCA TCGTGG CCGGC GCCTC CTCGGA GTCC TTGGGGA CGG     120
AGCAGCGCGT CGT GGGGCGA GCGG CAGAAG TCCCG GGCCC AGAGCC CGGC CAGCAGG AGC     180
AGTTGGTCTT CGG CAGCGGG GATG CTGTGG AGCTG AGCTG TCCCC CGCCC GGGGGT GGTC     240
CCATGGGGCC CAC TGTCTGG GTCA AGGATG CACA GGGCT GGTGCC CTCG GAGCGTG TCC      300
TGGTGGGGCC CCA GCGGCTG CAGG TGCTGA ATGCC TCCCA CGAGGA CTCC GGGGCCT ACA     360
GCTGCCGGCA GCG GCTCACG CAGC GCGTAC TGTGC CACTT CAGTGT GCGG GTGACAG ACG     420
CTCCATCCTC GG GAGATGAC GAA GACGGGG AGGA CGAGGC TGAGG ACACA GGTGTG GACA     480
CAGGGGCCCC TTA CTGGACA CGGC CCGAGC GGATG GACAA GAAGCT GCTG GCCGTGC CGG     540
CCGCCAACAC CGT CCGCTTC CGCT GCCCAG CCGCT GGCAA CCCCAC TCCC TCCATCT CCT     600
GGCTGAAGAA CGG CAGGGAG TTCC GCGGCG AGCAC CGCAT GGAGG GCATC AAGCTG CGGC     660
ATCAGCAGTG GAG CCTGGTC ATGG AAAGCG TGGTG CCCTC GGACCG CGGC AACTACA CCT     720
GCGTCGTGGA GAA CAAGTTT GGCA GCATCC GGCAG ACGTA CACGCT GGAC GTGCTGG AGC     780
GCTCCCCGCA CCG GCCCATC CTGC AGGCGG GGCTG CCGGC CAACCA GACG GCGGTGC TGG     840
GCAGCGACGT GG AGTTCCAC TGC AAGGTGT ACAG TGACGC ACAGC CCCAC ATCCAG TGGC     900
TCAAGCACGT GGA GGTGAAC GGCA GCAAGG TGGGC CCGGA CGGCAC ACCC TACGTTA CCG     960
TGCTCAAGAC GGC GGGCGCT AACA CCACCG ACAAG GAGCT AGAGGT TCTC TCCTTGC ACA    1020
ACGTCACCTT TGA GGACGCC GGGG AGTACA CCTGC CTGGC GGGCAA TTCT ATTGGGT TTT    1080
CTCATCACTC TGC GTGGCTG GTGG TGCTGC CAGCC GAGGA GGAGCT GGTG GAGGCTG ACG    1140
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AGGCGGG   1147

SEQ ID NO:5:

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GACGGATCGG GAGATCTCCC GATCCCCTAT GGTCGACTCT CAGTACAATC TGCTCTGATG    60
CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG   120
CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC   180
TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT   240
GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGTC ATTAGTTCAT AGCCCATATA   300
TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC   360
CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC   420
ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACTGCCCA CTTGCAGTA CATCAAGTGT    480
ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT   540
ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA   600
TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG   660
ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC   720
AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG   780
GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA   840
CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC   900
GTTTAAACTT AAGCTTGGTA CCGAGCTCGG ATCCCCGTCG TGCATCTATC GAAGGTCGTG   960
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   GA GAT CCC GAG GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA    1007
      ASP PRO GLU GLU PRO LYS SER CYS ASP LYS THR HIS THR CYS PRO 15

   CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC    1055
   PRO CYS PRO ALA PRO GLU LEU LEU GLY GLY PRO SER VAL PHE LEU PHE 31

   CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC    1103
   PRO PRO LYS PRO LYS ASP THR LEU MET ILE SER ARG THR PRO GLU VAL 47

   ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC    1151
   THR CYS VAL VAL VAL ASP VAL SER HIS GLU ASP PRO GLU VAL LYS PHE 63

   AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG    1199
   ASN TRP TYR VAL ASP GLY VAL GLU VAL HIS ASN ALA LYS THR LYS PRO 79

   CGG GAG GAG CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC    1247
   ARG GLU GLU GLN TYR ASN SER THR TYR ARG VAL VAL SER VAL LEU THR 95

   GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC    1295
   VAL LEU HIS GLN ASP TRP LEU ASN GLY LYS GLU TYR LYS CYS LYS VAL 111

   TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC    1343
   SER ASN LYS ALA LEU PRO ALA PRO ILE GLU LYS THR ILE SER LYS ALA 127

   AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG    1391
   LYS GLY GLN PRO ARG GLU PRO GLN VAL TYR THR LEU PRO PRO SER ARG 143
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GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC   1439
ASP GLU LEU THR LYS ASN GLN VAL SER LEU THR CYS LEU VAL LYS GLY 159

TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG   1487
PHE TYR PRO SER ASP ILE ALA VAL GLU TRP GLU SER ASN GLY GLN PRO 175

GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC   1535
GLU ASN ASN TYR LYS THR THR PRO PRO VAL LEU ASP SER ASP GLY SER 191

TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG   1583
PHE PHE LEU TYR SER LYS LEU THR VAL ASP LYS SER ARG TRP GLN GLN 207

GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC   1631
GLY ASN VAL PHE SER CYS SER VAL MET HIS GLU ALA LEU HIS ASN HIS 223

TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGATCTAGAG   1677
TYR THR GLN LYS SER LEU SER LEU SER PRO GLY LYS   235

GGCCCGTTTA AAC CCGCTGA TCAG CCTCGA CTGTG CCTTC TAGTTG CCAG CCATCTG TTG   1737
TTTGCCCCTC CCC CGTGCCT TCCT TGACCC TGGAA GGTGC CACTCC CACT GTCCTTT CCT   1797
AATAAAATGA GGA AATTGCA TCGC ATTGTC TGAGT AGGTG TCATTC TATT CTGGGGG GTG   1857
GGGTGGGGCA GGA CAGCAAG GGGG AGGATT GGGAA GACAA TAGCAG GCAT GCTGGGG ATG   1917
CGGTGGGCTC TAT GGCTTCT GAGG CGGAAA GAACC AGCTG GGGCTC TAGG GGGTATC CCC   1977
ACGCGCCCTG TAG CGGCGCA TTAA GCGCGG CGGGT GTGGT GGTTAC GCGC AGCGTGA CCG   2037
CTACACTTGC CAG CGCCCTA GCGC CCGCTC CTTTC GCTTT CTTCC CTTCC TTTCTCGCCA   2097
CGTTCGCCGG CTT TCCCCGT CAAG CTCTAA ATCGG GGCAT CCCTTT AGGG TTCCGAT TTA   2157
GTGCTTTACG GCA CCTCGAC CCCA AAAAAC TTGAT TAGGG TGATGG TTCA CGTAGTG GGC   2217
CATCGCCCTG ATA GACGGTT TTTC GCCCTT TGACG TTGGA GTCCAC GTTC TTTAATA GTG   2277
GACTCTTGTT CCA AACTGGA ACAA CACTCA ACCC TATCTC GGTCT ATTCT TTTGAT TTAT   2337
AAGGGATTTT GGG GATTTCG GCCT ATTGGT TAAAA AATGA GCTGAT TTAA CAAAAAT TTA   2397
ACGCGAATTA ATT CTGTGGA ATGT GTGTCA GTTAG GGTGT GGAAAG TCCC CAGGCTC CCC   2457
AGGCAGGCAG AAG TATGCAA AGCA TGCATC TCAAT TAGTC AGCAA CCAGG TGTGGA AAGT   2517
CCCCAGGCTC CCC AGCAGGC AGAA GTATGC AAAGC ATGCA TCTCAA TTAG TCAGCAA CCA   2577
TAGTCCCGCC CCT AACTCCG CCCA TCCCGC CCCTA ACTCC GCCCAG TTCC GCCCATT CTC   2637
CGCCCCATGG CTG ACTAATT TTTT TTATTT ATGCA GAGGC CGAGGC CGCC TCTGCCT CTG   2697
AGCTATTCCA GAA GTAGTGA GGA GGCTTTT TTGG AGGCCT AGGCT TTTGC AAAAAG CTCC   2757
CGGGAGCTTG TAT ATCCATT TTCG GATCTG ATCAG CACGT GTTGAC AATT AATCATC GGC   2817
ATAGTATATC GGC ATAGTAT AATA CGACAA GGTGA GGAAC TAAACC ATGG CCAAGTT GAC   2877
CAGTGCCGTT CCG GTGCTCA CCGC GCGCGA CGTCG CCGGA GCGGTC GAGT TCTGGAC CGA   2937
CCGGCTCGGG TTC TCCCGGG ACTT CGTGGA GGACG ACTTC GCCGGT GTGG TCCGGGA CGA   2997
CGTGACCCTG TTC ATCAGCG CGGT CCAGGA CCAGG TGGTG CCGGAC AACA CCCTGGC CTG   3057
GGTGTGGGTG CGC GGCCTGG ACGA GCTGTA CGCCG AGTGG TCGGAG GTCG TGTCCAC GAA   3117
CTTCCGGGAC GCC TCCGGGC CGGC CATGAC CGAGA TCGGC GAGCAG CCGT GGGGGCG GGA   3177
GTTCGCCCTG CGC GACCCGG CCGG CAACTG CGTGC ACTTC GTGGCC GAGG AGCAGGA CTG   3237

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    CGTTTTCCGG GAC GCCGGCT GGAT GATCCT CCAGC GCGGG GATCT CATGC TGGAGT TCTT   3357
    CGCCCACCCC AAC TTGTTTA TTGC AGCTTA TAATG GTTAC AAATAA AGCA ATAGCAT CAC   3417
    AAATTTCACA AAT AAAGCAT TTTT TTCACT GCATT CTAGT TGTGGT TTGT CCAAACT CAT   3477
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    CAATGTATCT TAT CATGTCT GTAT ACCGTC GACCT CTAGC TAGAGC TTGG CGTAATC ATG   3537
    GTCATAGCTG TT TCCTGTGT GAA ATTGTTA TCCG CTCACA ATTCC ACACA ACATAC GAGC   3597
    CGGAAGCATA AAG TGTAAAG CCTG GGGTGC CTAAT GAGTG AGCTAA CTCA CATTAAT TGC   3657
    GTTGCGCTCA CTG CCCGCTT TCCA GTCGGG AAACC TGTCG TGCCAG CTGC ATTAATG AAT   3717
    CGGCCAACGC GCG GGGAGAG GCGG TTTGCG TATTG GGCGC TCTTCC GCTT CCTCGCT CAC   3777
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    AATACGGTTA TCC ACAGAAT CAGG GGATAA CGCAG GAAAG AACATG TGAG CAAAAGG CCA   3897
    GCAAAAGGCC AGG AACCGTA AAAA GGCCGC GTTGC TGGCG TTTTTC CATA GGCTCCG CCC   3957
    CCCTGACGAG CAT CACAAAA ATCG ACGCTC AAGT CAGAGG TGGCG AAACC CGACAG GACT   4017
    ATAAAGATAC CAG GCGTTTC CCCC TGGAAG CTCCC TCGTG CGCTCT CCTG TTCCGAC CCT   4077
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    CTCACGCTGT AGG TATCTCA GTTC GGTGTA GGTCG TTCGC TCCAAG CTGG GCTGTGT GCA   4197
    CGAACCCCCC GTT CAGCCCG ACCG CTGCGC CTTAT CCGGT AACTAT CGTC TTGAGTC CAA   4257
    CCCGGTAAGA CAC GACTTAT CGCC ACTGGC AGCAG CCACT GGTAAC AGGA TTAGCAG AGC   4317
    GAGGTATGTA GGC GGTGCTA CAGA GTTCTT GAAGT GGTGG CCTAAC TACG GCTACAC TAG   4377
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20
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    AAGGACAGTA TTT GGTATCT GCGC TCTGCT GAAGC CAGTT ACCTTC GGAA AAAGAGT TGG   4437
    TAGCTCTTGA TCC GGCAAAC AAAC CACCGC TGGTA GCGGT GGTTTT TTTG TTTGCAA GCA   4497
    GCAGATTACG CGC AGAAAAA AAGG ATCTCA AGAAG ATCCT TTGATC TTTT CTACGGG GTC   4557
    TGACGCTCAG TGG AACGAAA ACTC ACGTTA AGGGA TTTTG GTCATG AGAT TATCAAA AAG   4617
    GATCTTCACC TAG ATCCTTT TAAA TTAAAA ATGAA GTTTT AAATCA ATCT AAAGTAT ATA   4677
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25
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    CTGTCTATTT CGT TCATCCA TAGT TGCCTG ACTCC CCGTC GTGTAG ATAA CTACGAT ACG   4797
    GGAGGGCTTA CCA TCTGGCC CCA GTGCTGC AATG ATACCG CGAGA CCCAC GCTCAC CGGC   4857
    TCCAGATTTA TCA GCAATAA ACCA GCCAGC CGGAA GGGCC GAGCGC AGAA GTGGTCC TGC   4917
    AACTTTATCC GCC TCCATCC AGTC TATTAA TTGTT GCCGG GAAGCT AGAG TAAGTAG TTC   4977
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    GCCAGTTAAT AGT TTGCGCA ACGT TGTTGC CATTG CTACA GGCATC GTGG TGTCACG CTC   5037
    GTCGTTTGGT ATG GCTTCAT TCAG CTCCGG TTCCC AACGA TCAAGG CGAG TTACATG ATC   5097
    CCCCATGTTG TGC AAAAAAG CGGT TAGCTC CTTCG GTCCT CCGATC GTTG TCAGAAG TAA   5157
    GTTGGCCGCA GTG TTATCAC TCAT GGTTAT GGCAG CACTG CATAAT TCTC TTACTGT CAT   5217
    GCCATCCGTA AGA TGCTTTT CTG TGACTGG TGAG TACTCA ACCAA GTCAT TCTGAGA ATA   5277
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    TAGCAGAACT TTA AAAGTGC TCAT CATTGG AAAAC GTTCT TCGGGG CGAA AACTCTC AAG   5397
    GATCTTACCG CTG TTGAGAT CCAG TTCGAT GTAAC CCACT CGTGCA CCCA ACTGATC TTC   5457
    AGCATCTTTT ACT TTCACCA GCGT TTCTGG GTGAG CAAAA ACAGGA AGGC AAAATGC CGC   5517
    AAAAAAGGGA ATA AGGGCGA CACG GAAATG TTGAA TACTC ATACTC TTCC TTTTTCA ATA   5577
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40
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    TTATTGAAGC ATT TATCAGG GTTA TTGTCT CATGA GCGGA TACATA TTTG AATGTAT TTA   5637
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GAAAAATAAA CAA ATAGGGG TTCC GCGCAC ATTTC CCCGA AAAGTG CCAC CTGACGT C   5695

SEQ ID NO:6

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       ASP PRO GLU GLU PRO LYS SER CYS ASP LYS THR HIS THR CYS PRO PRO 16
       CYS PRO ALA PRO GLU LEU LEU GLY GLY PRO SER VAL PHE LEU PHE PRO 32
  5    PRO LYS PRO LYS ASP THR LEU MET ILE SER ARG THR PRO GLU VAL THR 48
       CYS VAL VAL VAL ASP VAL SER HIS GLU ASP PRO GLU VAL LYS PHE ASN 64
       TRP TYR VAL ASP GLY VAL GLU VAL HIS ASN ALA LYS THR LYS PRO ARG 80
       GLU GLU GLN TYR ASN SER THR TYR ARG VAL VAL SER VAL LEU THR VAL 96
       LEU HIS GLN ASP TRP LEU ASN GLY LYS GLU TYR LYS CYS LYS VAL SER 112
 10    ASN LYS ALA LEU PRO ALA PRO ILE GLU LYS THR ILE SER LYS ALA LYS 128
       GLY GLN PRO ARG GLU PRO GLN VAL TYR THR LEU PRO PRO SER ARG ASP 144
       GLU LEU THR LYS ASN GLN VAL SER LEU THR CYS LEU VAL LYS GLY PHE 160
       TYR PRO SER ASP ILE ALA VAL GLU TRP GLU SER ASN GLY GLN PRO GLU 176
       ASN ASN TYR LYS THR THR PRO PRO VAL LEU ASP SER ASP GLY SER PHE 192
 15    PHE LEU TYR SER LYS LEU THR VAL ASP LYS SER ARG TRP GLN GLN GLY 208
       ASN VAL PHE SER CYS SER VAL MET HIS GLU ALA LEU HIS ASN HIS TYR 224
       THR GLN LYS SER LEU SER LEU SER PRO GLY LYS                      235
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Both FR3exFc and FR1exFc soluble receptors were demonstrated to be expressed to a high
level in transiently transfected 293T cells (T-cell antigen infected human embryonic kidney
20   293 cells). The observation that both soluble receptors remain bound to heparin-coated wells
even following extensive washes led the laboratory of the present inventors to try to purify
the proteins with the commercial heparin-Sepharose™ resin (Pharmacia). One hundred ml
volume supernatants, harvested 48 hours post transfection with either FR3exFc or FR1exFc
coding plasmids, were incubated overnight at 4°C with 1 ml heparin-Sepharose™ resin. The
25   resin was washed and then subjected to PBS supplemented with increasing concentration of
NaCl. Aliquots of each fraction were analyzed by 7.5% SDS-PAGE stained with GelCode
(Pierce) demonstrating a purification profile of more than 90% homogeneity and a peak
elution at 400 mM NaCl for FR3exFc (Fig. 3; T=total protein, U=unbound fraction,
W=wash). In contrast, FR1exFc was hardly retained on the resin. This result was confirmed
30   by Western analysis of the same fractions with anti-FGFR1ex antibodies demonstrating that
most of FR1exFc is in the unbound fraction (not shown).

Functional analysis of FR3exFc and FR1exFc showed that both compete efficiently for FGF9
binding and stimulating FGFR3, thus, demonstrating their potential as inhibitors of FGFRs
function and as a target (FR3exFc) for selecting FGFR3 inhibitory molecules.

Neutralizing effect of soluble receptors

The ability of hFR3-TDhis and FR3exFc to inhibit FGF-dependent FDCP-R3 cell proliferation was compared. Both soluble receptors inhibited FDCP-R3 cell proliferation, however, FR3exFc was about 60 times more potent than hFR3TDhis (Fig. 4; legend: ♦-

5   FDCP-FR3$^{23-374}$TDhis on FDCP-FR3 cells + FGF9, ■-FR3exFc on FDCP-FR3 cells + FGF9, ▲- FDCP-FR3$^{23-374}$TDhis on FDCP-FR3 cells + IL, X- FR3exFc on FDCP-FR3 cells + IL3). Neither had an effect on FDCP cells stimulated with IL3. The fact that FR3exFc is entirely in dimeric form whereas only a small proportion (1/10) of hFR3$^{23-374}$TDhis is in a dimeric form might explain, at least in part, this difference.

10   **Example 3: Screening for Antibodies**

Panning and first screening of Ab Binding Characterization

The screening strategies to identify Fabs from the Human Combinatorial Antibody Library (HuCAL®), developed at MorphoSys, Munich, Germany and disclosed in WO 97/08320, US patent 6,300,064, and Knappik et al., (2000), the entire contents of which are incorporated

15   herein by reference, using soluble dimeric forms of the extracellular domain of the FGFR3 receptor are shown in Table 2.

TABLE 2

Panning Strategies

	Panning Round 1	Panning Round 2	Panning Round 3
Screen 1	FR3-TDhis	HEK293	FR3-TDhis
Screen 2	FR3exFc captured with mouse anti-human IgG	RCJ-FR3ach	FR3exFc captured with mouse anti-human IgG
Screen 3	FR3-TDhis (Round 1 of panning 1)	RCJ-FR3ach & RCJ-FR3wt	FR3exFc Captured with mouse anti-human IgG

The screening was carried out, for example in Screen 1, by coating the wells of a 96 well

20   plate with hFR3$^{23-374}$TDhis (FR3-TDhis), panning with the bacteriophage library and

selecting the positive clones. The positive clones were then tested on HEK293 (293, human embryonic kidney) cells, expressing endogenous FGFR3. The positive clones were selected and rescreened on FR3-TDhis. Two additional similar screenings were carried out as shown in Table 2. In screen 2 the first and third pannings were carried out with the FR3exFc antigen

5   and the second panning carried out with RCJ cells expressing a mutant (achondroplasia) form of FGFR3.

An overview of the number of initial hits and of the candidate clones is shown in Table 3.

Table 3

Overview of Screenings 1, 2 and 3 on FGFR3

	screened clones	primary hits	sequenced clones	consolidated candidate clones (ELISA & FACS)
Screen 1	1076	208	69	15 MSPRO 1-15
Screen 2	864	300	32	22 MSPRO 20-33 and 52-59
Screen 3	768	487	52	11 MSPRO 40-50

10   <u>Sequence and Vector Data</u>

A plasmid map and sequence (SEQ ID NO:52) of the dHLX-MH vector are presented in Fig. 28A and 28B.

Figure 29A shows the plasmid map of the phage display vector used in accordance with the present invention. Figure 29B is the corresponding sequence and restriction digest map (SEQ

15   ID NO:53).

Figure 30 displays the polynucleotide sequences of the specific VL and VH domains of MSPRO2 (SEQ ID NO:74 and 84); MSPRO11 (SEQ ID NO:70 and 85), MSPRO12 (SEQ ID NO:75 and 89); MSPRO21 (SEQ ID NO:67 and 78); MSPRO24 (SEQ ID NO:64 AND 79); MSPRO26 (SEQ ID NO:71 AND 86); MSPRO28 (SEQ ID NO:62 AND 80); MSPRO29

20   (SEQ ID NO:65 AND 87); MSPRO54 (SEQ ID NO:73 AND 82); MSPRO55 (SEQ ID NO:69 AND 83); MSPRO59 (SEQ ID NO:76 AND 91). The sequences include the framework domains 1-4 and the CDR domains 1-3. SEQ ID NO:61, 63, 66, 68, and 73

denote the polynucleotide sequences of the parent VL (kappa or lambda) strands. SEQ ID
NO:77, 81, 88 and 90 denote the polynucleotide sequences of the VH parent strands.

Example 4:Analysis of Fabs identified by first screening.

Specificity of Antibody recognition

5   The first screening yielded 15 different Fabs that specifically recognize FGFR3 *in vitro* and
on the cell surface. Fourteen of these were produced and sent to ProChon for further analysis.
LY6.3, an anti-lysosyme antibody, was isolated from the same library and serves as a control.
ELISA analysis, according to the following protocol was carried out to determine the
specificity of the isolated Fabs for FGFR3 or FGFR1.

10   Fab-FR3/Fc Binding Assay

MaxiSorp ELISA plates were coated with 100 µl anti-human Fc (10 µg/ml) in bicarbonate
overnight at 4°C. Wells were washed five consecutive times with a PBS solution containing
0.1% Tween 20 (PBST). The well surface was blocked with 250 µl PBST+3%BSA (blocking
solution) for 1 hour at 37°C. This was followed by capturing 1 µg of FGFR/Fc for 1 hour at

15   room temperature. To assess the antibody binding to the captured FGFR/Fc, 1 µg each of the
tested Fabs was incubated in 100 µl blocking solution per well 1 hour at room temperature
Wells were washed 5 times with PBST. Reaction was initiated with the addition of 100 µl of
0.8µg/ml goat anti-human Fab-HRP diluted in blocking solution, subsequently washed and
detected with TMB substrate (Pierce). The absorbance was measured at 450 nm. A

20   comparison of ELISA analyses done in the laboratory of the present inventors (Prochon) and
at MorphoSys is presented in the following Table 4.

25

30

TABLE 4

ProChon	MorphoSys			
	FR1/Fc	FR3/Fc	FR1/Fc	FR3/Fc
MS-PRO1	++	++	+/-	+
MS-PRO2	-	++	-	++
MS-PRO3	+	++	-	++
MS-PRO4	-	+	-	++
MS-PRO5	-	++	+/-	+
MS-PRO6	-	++	-	+
MS-PRO7	-	++	-	+
MS-PRO8	+	++	-	+
MS-PRO9	-	+/-	+/-	+
MS-PRO10	+	++	-	++
MS-PRO11	-	+/-	+	++
MS-PRO12	-	+/-	-	++
MS-PRO13	-	+/-	+/-	+
MS-PRO14	-	-	-	+
LY6.3 (control)	-	-		

In most cases, the data generated at Morphosys and in the laboratory of the present inventors are in agreement. However, some Fabs behave differently. For example, MS-PRO3 and 10 were found to be completely FGFR3 specific under Morphosys conditions. In the laboratory of the present inventors, both show considerable cross-reaction with FGFR1. The FACS analysis, done at Morphosys, supports the Prochon results for MS-PRO3 but not for MS-PRO10. Taking into account the potency and specificity of the Fabs, MS-PRO2 has the highest score according to these preliminary data.

Example 5: Affinity of Fab to FGFR3

The affinity measurements were performed by BIAcore according to the standard procedure recommended by the supplier (Pharmacia). The anti-Fc antibody was coupled via the EDC/NHS chemistry to the chip and subsequently FGFR3 was captured. The Fabs of the invention were then bound to this surface.

Table 5 shows a comparison of affinities of Fabs candidates to FGFR3 as determined by BIAcore and by FACS-scatchard.

Table 5

Comparison of Antibody Affinities to FGFR3
determined by BIAcore and FACS-Scatchard

Fab clone	BIAcore [nM]	Indirect FACS-Scatchard [nM]
MSPRO2	37 ± 10	43
MSPRO11	4 ± 2	4
MSPRO12	14 ± 2	6.5
MSPRO21	9 ± 2	0.6
MSPRO24	10 ± 2	0.3
MSPRO26	4 ± 1	1.4
MSPRO28	9 ± 0.4	0.3
MSPRO29	6 ± 4	0.4

Table 1E shows the affinity as determined by BIAcore for the Fab candidates shown in Table 5 converted into the Fab mini-antibody format, Fab-dHLX-MH, where a dimer of the Fab monomer is produced after insertion into an expression vector as a fusion protein.

Table 6 shows the results of a competition assay wherein each MSPRO Fab was bound to the FGFR3 at a concentration of 500nM or 1, 000 nM and coinjected in pairs with the other MSPRO Fabs. The (-) indicates binding to the same or nearby epitope while (+) indicates binding to different epitope. The results show that MSPRO2 and12 bind to the same or nearby epitope while MSPRO11, 21, 24, 26, 28 and 29 bind to an epitope different from that of MSPRO2 or 12.

Example 6: Specific Neutralizing Activity of the Antibodies

A: FDCP Cell Proliferation Assay

The FDCP cell line is a murine immortalized, interleukin 3 (IL3) dependent cell line of myelocytic bone marrow origin, which does not express endogenous FGF Receptors (FGFR).

Upon transfection with FGFR cDNA, the FDCP cell line exhibits an FGF dose dependent proliferative response that can replace the dependence on IL3. FDCP cell lines, transfected with FGFR cDNAs can therefore be used to screen for specific inhibitors or activators of FGFR, as well as for analyzing FGFR signaling. The FDCP cell response to various ligands

5   was quantitated by a cell proliferation assay with XTT reagent (Cell Proliferation Kit, Biological Industries Co.). The method is based on the capability of mitochondrial enzymes to reduce tetrazolium salts into soluble colored formazan compounds which can be quanititated and is indicative of cell viability. Specifically, FDCP cells expressing FGFR3IIIb, FGFR3IIIc or FGFR1 were grown in "full medium" (Iscove's Medium

10   containing 2ml glutamine, 10% FCS, 100ug/ml penicillin, 100ug/ml streptomycin) supplemented with 5ug/ml heparin and 10ng/ml FGF9. Cells were split every 3 days and kept in culture no more than one month. One day prior to the experiment, the cells were split. Before the experiment, the cells were washed 3 times (1000 rpm, 6 min) with full medium. Later, the cells were resuspended and counted with Trypan Blue. Twenty thousand (20,000)

15   cells /well were added to wells in a 96-well plate in 50ul in full medium containing 5 ug/ml heparin. Conditioned medium was added in an additional volume of 50ul full medium containing FGF9 at varying concentrations to a final volume of 100ul. A primary stock solution (usually 2x the higher concentration) of the antibody (or Fabs) was prepared in Iscove's+++ containing 5μg/ml heparin and 2.5ng/ml FGF9 or IL-3 (final concentration 1.25

20   ng/ml). Dilutions were filtered in a 0.2 μm syringe nitrocellulose filter blocked first with 1mg/ml BSA and washed then with Iscove's+++. Aliquots of requested serial dilutions were prepared. Dilutions were kept on ice until use. 50 μl of the corresponding 2x final concentration was added to each well and the plate was incubated at 37^{0}C for either 40 hours or either 64 hours. After incubation, the reaction was developed as follows: 100 μl of

25   activator solution was added to 5 ml XTT reagent and mixed gently. 50 μl of mixture was added to each well. Optical density (OD) at 490 nm at this point gave the zero time reading. Cells were then incubated at 37^{0}C for 4 hours (in the case of a 40 hour incubation) or 2 hours (in the case of a 64 hour incubation) and proliferation was measured by O.D. at 490 nm (A490).

30   It is noted that the assay is successful when the O.D. of untreated control growing with saturated amounts of FGF (10 and 20 ng/ml) is at least 1.3 O.D. units. Furthermore, it is noted that the background of wells with no cells should be 0.2-0.35 O.D. units and that the

O.D. absorbance of 1.25 ng/ml FGF9 should not be less than 40% of the O.D. absorbance achieved with saturated FGF 9 concentration (10 and 20 ng/ml). Specific inhibition of FGF and FGF receptor mediated proliferation should always be accompanied with lack of any inhibition of the same antibody concentration on IL-3 dependent cell proliferation.

5   The following FDCP cell lines were used:

*FDCP-C10: FDCP cells transfected with the human wild-type FGF receptor 3IIIc.

*FDCP-R3: FDCP cells transfected with the human wild-type FGF receptor 3IIIb.

*FDCP-R1: FDCP cells transfected with the human wild-type FGFR1.

*FDCP-F3Ach: FDCP cells infected with human FGFR3 mutated at amino acid Glycine 380

10   to Arginine (G380R), analogous to the most common human achondroplasia mutation.

B: Neutralizing activity

The neutralizing activity of the antibodies was measured by the aforementioned cell proliferation analysis in FDCP-FR3 and FDCP-FR1 cell lines. Increasing amounts of the indicated Fabs (MSPRO 2, 3 and 4) were added to FDCP-FR3 (closed triangle ▲(2), star *

15   (3), and circle ● (4)) or FDCP-FR1 (diamond ♦ (2), square ■ (3) and open triangle Δ(4)) grown in the presence of FGF9 (Fig. 5). Two days later, an XTT proliferation assay was performed. While none of the Fabs inhibited FDCP-FR1 cell proliferation, MSPRO2 and 3 inhibited FDCP-FR3 proliferation with a similar IC50 of about 1.0 μg/ml (Fig. 5). In contrast, MS-PRO4 had no inhibitory effect on FDCP-FR3 proliferation. These data are in

20   agreement with those generated at Morphosys. The rest of the Fabs were similarly analyzed on FDCP-FR3 expressing cells. Increasing amounts of the indicated Fabs were added to FDCP-FR3 grown in the presence of FGF9 (Fig. 6). The results of the proliferation assay done at Morphosys and at Prochon are compared in Table 6. (NA- data not available)

25

30

Table 6

	Prochon		Morphosys	
	FDCP-FR1	FDCP-FR3	FDCP-FR1	FDCP-FR3
MSPRO1	-	++	NA	NA
MSPRO2	-	++	NA	++
MSPRO3	-	++	NA	++
MSPRO4	-	-	NA	-
MSPRO5	-	+	NA	+
MSPRO6	-	-	NA	+/-
MSPRO7	-	++	NA	+
MSPRO8	-	+/-	NA	+/-
MSPRO9	-	+	NA	+
MSPRO10	-	+	NA	NA
MSPRO11	-	+++	NA	++
MSPRO12	-	+++	NA	+++
MSPRO13	-	-	NA	NA
MSPRO14	-	-	NA	NA
LY6.3	-	-	NA	NA

As shown in Table 6, there is an excellent agreement between the Prochon and Morphosys data. About half of the Fabs show considerable neutralizing activity, MSPRO12 being the most potent. Most of the inhibitory Fabs performed well in the binding assay (Table 4), with MSPRO11 and MSPRO12 being the exception to the rule, however, clearly remain good candidates to pursue. None of the Fabs (including those that crossreact with FGFR1) inhibited FGF-dependent FDCP-FR1 proliferation. In addition, FDCP-FR3 grown in the presence of IL3 were not affected by any of the Fabs.

An additional 20 new Fabs were selected from the second panning done at Morphosys. Three of these new Fabs (MSPRO52, MSPRO54 and MSPRO55) were subjected to the FDCP cell proliferation test and all were found to neutralize the receptor (Fig. 7A). Interestingly (and in

accord with MorphoSys affinity data), one Fab (MSPRO54) showed strong neutralizing activity against FGFR1 (Fig. 7B).

Example 7: Receptor Expression and Activation in RCJ Cells

RCJ cell assay

5   RCJ cells (fetal rat calvaria-derived mesenchymal cells, RCJ 3.1C5.18; Grigoriadis, 1988) were generated to express various FGF Receptors an inducible manner, in the absence of tetracycline. The RCJ-M14 line (RCJ-FR3ach) expresses FGFR3-ach380 mutant upon induction by the removal of tetracycline. The cells were incubated in low serum after which FGF was added to stimulate receptor function and signaling. The cells were lysed and the

10   receptor level, receptor activation and signaling are assessed by Western with anti-FGFR3 (Santa Cruz), anti-phospho-tyrosine (Promega), and anti-active ERK (or JNK) (Promega) respectively.

RCJ-M14 cells were grown in α-MEM supplemented with 15% fetal calf serum, 1x penicillin/streptomycin/nystatin, 1x glutamine, 600 μg/ml neomycin, 2 μg/ml tetracycline, 50

15   μg/ml hygromycin B to subconfluence. The medium was aspirated off and the cells washed with trypsin, 1 ml/10 cm dish, then trypsinized with 0.5 ml/10 cm dish. The cells were resuspended in 10 ml α-MEM supplemented with 15% fetal calf serum, 1x penicillin/streptomycin/nystatin, 1x glutamine, 600 μg/ml neomycin, and 2 μg/ml tetracycline.

20   Sixty thousand ($6x10^5$) cells/well were seeded in a 6-well dish. Alternatively, twice that number may be seeded. The cells were washed thrice 24 hours later (or 8 hours later if twice the amount of cells are seeded) with 1 ml α-MEM, and then incubated with α-MEM supplemented with 15% fetal calf serum, 1x penicillin/streptomycin/nystatin, and 1x glutamine (induction medium) for 16 hours. Cells were washed thrice with 1 ml α-MEM

25   and allowed to grow for 4 additional hours in 1 ml of 0.5% exhausted serum (prepared by diluting the induction medium X30 with α-MEM).

FGF9 (1 ng/ml) was added for 5 minutes and cells are then placed on ice. The cells were washed twice with ice-cold PBS and then lysed with 0.5 ml lysis buffer. The cells are scraped into an eppendorf tube, vortexed once and placed on ice for 10 minutes. The lysate

30   was microcentrifuged 10 minutes at 4^0C and the cleared lysate transferred into a fresh Eppendorf tube.

The protein content was determined by Bradford or DC protein assay (Bio-Rad, cat# 500-0116 - see manufacture instructions). Total protein aliquots, supplemented with 1/5 volume of 5x sample buffer, were boiled for 5 minutes and stored at -20⁰C until ready to load on gel. In parallel an immunoprecipitation (IP) assay was performed, 10 μl anti- FGFR3 antibodies

5   were added to the rest of the lysates and incubated for 4 hours at 4⁰C. 40 μl protein A-Sepharose was added and incubated for 1 hour at 4⁰C with continuous shaking. Afterwards, the mixture was microcentrifuged 15 seconds, and the fluid was aspirated, carefully leaving a volume of ~30 μl above the beads. The beads were washed 3 times with 1 ml lysis buffer. At this step, the protease inhibitor mix is omitted from the buffer.

10   After the final wash, 15 μl of 5x sample buffer was added, samples were boiled 5 minutes and stored at -20⁰C until ready to load onto gel. Samples were loaded on 7.5% SDS-PAGE, cast on a Mini-PROTEAN II electrophoresis cell, and run at 100 V through the upper gel and at 150 V through the lower gel. Proteins were transferred onto nitrocellulose sheet using the Mini trans-blot electrophoretic transfer cell at 100 V for 75 minutes or at 15 V overnight.

15   The lower part of the total lysate Western blots was probed with anti-active MAPK (ERK) and the upper part is probed with anti-phosphotyrosine, both diluted 5×10^3. The IP lysate Western blots were probed with anti-anti-phosphotyrosine (R&D Systems). Hybridization was detected by ECL following the manufacturer's instructions.

BIAcore and proliferation analyses done at MorphoSys showed that among the new Fabs,

20   MS-PRO54 is highly cross reactive with FGFR1. To further test the cross reactivity of the new Fabs, RCJ cells expressing either FGFR3ach (RCJ-M14; M14 on figure 9A) FGFR3 wild type (W11 on figure 9B), FGFR1 (R1-1 on figure 9C) or FGFR2 (R2-2 on figure 9D) were incubated with increasing amount of MS-PRO54 and MS-PRO59 for 1 hour. FGF9 was added for 5 minutes and cell lysates were analyzed by Western for pERK activation (Figs.

25   8A-B, 9A-9D). Figure 8A shows that MSPRO2 and MSPRO12 block FGFR3 receptor activation in W11 and RCJ-FR3ach expressing cells. Furthermore MSPRO13 was able to block FGFR1 activation while none of the Fabs blocked FGFR2 activation. Figures 8B and 9A-9D show the results of several Fabs on RCJ expressing wildtype FGFR3 (8B) or the different FGFR types. MSPRO29 appeared as the best FGFR3 blocker and was also effective

30   in blocking FGFR1 (Fig. 9c); however, MSPRO54 was the most effective Fab against FGFR1. None of the Fabs significantly inhibited FGFR2 activity. There are only a few amino acid residues, within the third Ig domain, that are shared by FGFR3 and FR1 but not by FR2.

Making mutants at these sites should clarify their role in Fab-receptor binding. Figure 8B depicts the dose effect of MS-PRO12, 29 and 13, stimulated with FGF9 and analyzed by Western blot using anti-ERK antibodies. . MSPRO29 strongly inhibits FGFR3 activation (5ug), MSPRO12 has an inhibitory effect but at a higher concentration (50 ug).

5   **Example 9: Epitope mapping of selected Fabs**

Constructs containing cDNAs that code for segments of the extracellular domain of FGFR3 were generated (Fig. 10). D2 comprises Ig domain 2, D2-3 comprises Ig domains 2 and 3 and D1-3 comprises Ig domains 1, 2 and 3. These include pChFR3^{D2}Fc that codes for Ig-like domain 2 of FGFR3 and pChFR3^{D2,3}Fc that codes for domain 2 and 3, both as human Fc

10   fusions. The corresponding chimeric proteins, as well as the control hFR3exFc (containing domains 1, 2 and 3) were anchored to an ELISA plate coated with α human Fc antibody. A panel of 8 best Fabs, MSPRO2, 11, 12, 21, 24, 26, 28 and 29, were added, and bound Fab was determined with HRP-α human Fab (Fig. 11). The results in Fig. 11 demonstrate that MSPRO2 (speckled bar) and MSPRO12 (hatched bar) differ from the other tested Fabs. Both

15   bind to the Ig like domain 2 while the others require domain 3 for binding. It was then tested whether or not Fabs that belong to the second group would distinguish the FGFR3IIIc isoform from the FGFRIIIb from. FDCP-FR3IIIb or FDCP-FR3IIIc cells were incubated in the presence of 1.25 ng/ml FGF9 with increasing doses of either MSPRO12 or MSPRO29. Ly6.3 was included as control. After 2 days in culture, cell proliferation was measured with

20   the XTT reagent. Clearly, MSPRO29 (open triangle) was completely ineffective against the IIIb isoform (Fig. 12). In contrast, MSPRO12 (square on hatched or solid lines) was equally effective against both isoforms. These data suggest that residues that differ between the two isoform are critical for MSPRO29 (and probably also for the other Fabs in the same group) FGFR3 binding.

25   Domains in FGFR3 recognized by the new Fabs.

In agreement with data generated at Morphosys, MSPROs can be divided into 2 groups, one that includes Fabs that bind the FGFR3 Ig II domain (MSPRO2 and 12) and a second with members that require the Ig III domain for binding (MSPRO11, 21, 24, 26, 28, and 29). To classify the new Fabs obtained from the last screen performed at Morphosys, as well as some

30   previously obtained Fabs, a proliferation assay of FDCP cells expressing either FR3IIIb or FR3IIIc was performed. The cells were incubated in the presence of 10 (IIIb) or 5 (IIIc)

ng/ml FGF9 with increasing doses of the indicated Fabs. After 2 days in culture, cell proliferation was measured with the XTT reagent.

In agreement with Morphosys data, MSPRO59 efficiently inhibited both FDCP-FR3IIIb (Fig. 13A) and FDCP-FR3IIIc cells (Fig. 13B) while MSPRO21, 24, 26, 28, 29 and 54 inhibited

5   FDCP-FR3IIIc proliferation only.

Example 10: Bone culture

Radiolabeled MSPRO29 was used to determine whether or not MSPRO Fabs can enter the bone growth plate.

To determine the effect of iodination on Fab activity, 50 µg of MSPRO29 was first labeled

10   with cold iodine using Pierce IodoGen coated tubes. The process was carried out either without iodine, with 0.04 mM or with 1 mM NaI. MSPRO29 was then purified through a sephadex G-50 column. The ability of the modified Fab to bind FGFR3 was determined by ELISA. MaxiSorp wells were coated with anti-human Fc. FGFR3/Fc (checkered bars) was then anchored to the wells. In parallel, a similar set of wells was left in blocking buffer only

15   (no FR3/Fc, hatched bars). The unmodified (no I) or the modified MSPRO29 (low for that labeled with 0.04 mM NaI (low) and high for that labeled at 1 mM NaI (high); 2 G-50 fractions each) were added at approximately 5 µg/well and binding was measured with anti-human Fab. Fresh MSPRO29 and buffer alone were included as controls (Fig. 14)..

MSPRO29 labeled in the presence of 0.04 mM NaI showed equal binding to the receptor as

20   compared to the control unmodified Fab MSPRO29 labeled in the presence of 1 mM NaI (high I) also bound the receptor, however, the noise level of this sample was as high as the signal itself suggesting that at the high Iodide concentration the Fab was inactivated.

The neutralizing activity of the modified Fab was tested in a proliferation assay using FDCP-FR3 (C10) (Fig. 15). FDCP-FR3 (C10) cells were treated with the indicated amount of

25   labeled or unlabeled (without I) MSPRO29. The proliferation rate of the cells was determined by XTT analysis. The Fab was labeled at either 0.04 mM (Low) or 1 mM NaI (High). Two G-50 fraction (I and II) were analyzed. Fresh MSPRO29 and buffer alone (mock) were included as controls.

This experiment showed that MSPRO29, labeled at 0.04 mM NaI, kept its activity almost

30   entirely while that labeled at 1 mM NaI lost its activity completely. MS-PRO29 was labeled with 1 mCi ^{125}I. The specific activity of the Fab was 17 µCi/µg.

Ex vivo distribution of ^{125}I MSPRO29 in bone culture

Femora prepared from newborn mice were incubated with 2 μg ^{125}I-MSPRO29 (17 μCi/μg)
or ^{125}I-Ly6.3 (20 μCi/μg) for 1, 3 or 5 days in culture. Then, sections were processed for
radiomicroscopy. After 3 days in culture, MSPRO29 was predominantly visualized at the

5   higher hypertrophic zone and to a lesser extent at the secondary ossification region (Figs.
16A-16F). Hematoxylin-eosin staining of growth plate treated with radiolabelled MS-PRO29
or Ly6.3 (Figs. 16A and 16D, respectively) x100 magnification. Radiomicoscopic sections
of growth plate treated with radiolabelled MS-PRO29 or Ly6.3 (Figs. 16B and 16E) at X100
magnification. Figs. 16C and 16F are the same as Figs. 16B and 16E but at x400

10   magnification. The arrow in figure 16C indicates the location of the specific binding of the
radiolabelled MS-PRO29 to the higher hypertrophic zone of the growth plate.

As compared to MSPRO29, the control Ly6.3 Fab was weakly and evenly distributed
throughout the whole growth plate. At day 1 in culture, the signal was weaker but with
similar distribution pattern. This distribution also holds at 5 days in culture with a less

15   favorable signal to noise ratio (data not shown). This clearly demonstrates that MSPRO29
binds FGFR3 in our target organ.

Example 11: Neutralizing Activity on Constitutively Activating Receptors

The inhibitory activity of MSPRO antibodies on ligand-dependent and ligand-independent
FDCP proliferation expressing FGFR3 Achondroplasia mutation was tested.

20   A proliferation assay was carried out using FDCP-FR3wt (C10) or FDCP-FR3ach cells
incubated with 1.25 or 5 ng/ml FGF9 respectively and with increasing amounts of MSPRO54
or MSPRO59. As shown in Fig. 17, both MSPRO54 (diamond) and 59 (square) antibodies
neutralize the mutant receptor. Few of the FDCP-FR3ach acquired ligand independent cell
proliferation due to the high expression of the FGFR3ach mutation.

25   FDCP cells that express the achondroplasia FGFR3 (FDCP-FR3ach) and proliferate
independently of ligand were incubated with the indicated amount of MSPRO12, 29, 59 or
the control Ly6.3. Two days later, cell proliferation was determined by an XTT analysis.
When inhibition of cell proliferation by the MS-PRO 12, 29, 54 and 59 were tested, only the
antibodies 12 and 59 (the only Ab which recognized D2 domain) inhibited the ligand-

30   independent cell proliferation (Figs. 18A and 18B). Previously, the activity of MSPRO Fabs
generated in the first and second screens (MSPRO1-15 and MSPRO21-31, respectively) by
XTT analysis of FDCP-FR3ach cells were tested. These cells, when generated, show ligand-

dependent proliferation. With time, however, they acquired a ligand-independent ability to proliferate. Accordingly, neutralizing Fabs were able to block the ligand-dependent, but not the ligand-independent, proliferation of these cells. To show whether this is also true for the new batch of Fabs, FDCP-FR3ach cells, which is the FDCP-dervied cell line that expresses a

5   constitutive FGFR3-G380R (Ach), were subjected to XTT analysis in the presence of MSPRO59 and MSPRO29. Surprisingly, and in contrast to the ineffective MSPRO29 (triangle), MSPRO59 (diamond) completely blocked cell proliferation (Fig. 18B). Whether other Fabs that, like MSPRO59, bind to the second Ig like domain would also inhibit FDCP-FR3ach cell proliferation was tested next. Indeed, it was found that MSPRO12 strongly

10   inhibits the constitutive cell proliferation. However, the third member in this family, MSPRO2, had no effect on either the constitutive or the ligand-dependent cell growth, suggesting that the Fab may have lost its neutralizing activity (not shown).

Example 12: RCS Chondrocyte Culture

Effect of Fabs on growth arrest of RCS Chondrocytes

15   RCS is a rat chondrosarcoma derived cell line expressing preferentially high levels of FGFR2 and FGFR3 and low levels of FGFR1 (Sahni, 1999). In this cell line FGFR functions as an inhibitor of cell proliferation similar to its expected role in the achondroplasia phenotype. Analysis of RCS cell proliferation mediated by the addition of different molecules of the invention, showed that MSPRO54 and MSPRO59 were able to restore cell proliferation.

20   The screening was performed on RCS parental cells in 96 wells plates. Cells were seeded at a concentration of 2,000 cells/well. The following day 10ng/ml FGF-9 and 5µg/ml heparin were added to the cells. 50ug/ml of the antibodies were added. Positive and negative controls for cell proliferation are included in this assay at the same concentrations as the tested molecules. On the fourth day of incubation, plates were observed under the microscope. If all

25   cells were viable, no quantitative assay to measure the effect of the variants was performed. If cell death was observed, the Cy-Quant assay kit is used to measure the amount of the cells. The results are measured in a fluoro ELISA reader. Figure 19 shows the ELISA results in bar graph form. Untraeted cells are shown speckled, ligand treated cells are shown in gray, control antibody (LY6.3)treated cells are in blak while MSPRO54 and MSPRO59 treated

30   cells are shown in hatched otr checkered bars, respectively.

Example 13: _Ex vivo_ Bone Culture

The femoral bone cultures were performed by excising the hind limbs of 369-mice, heterozygous or homozygous mice for the achondroplasia G369C mutation (age P0). The limbs were carefully cleaned up from the surrounding tissue (skin and muscles) and the

5   femora exposed. The femora were removed and further cleared from tissue remains and ligaments. The femora were measured for their initial length, using a binocular with an eyepiece micrometer ruler. The bones were grown in 1 ml of medium in a 24 well tissue culture dish. The growing medium is α-MEM supplemented with penicillin (100 units/ml), streptomycin (0.1 mg/ml) and nystatin (12.5 units/ml). In addition, the medium contains BSA

10   (0.2%), α-glycerophosphate (1 mM) and freshly prepared ascorbic acid (50 µg/ml). The bones were cultured for 15 days. Measurements of bone length and medium replacement were performed every three days.

At the end of the experiment, the growth rate of the bones was determined. The growth rate of bones is calculated from the slope of a linear regression fit on the length measurements

15   obtained from day 3 to 9.

The results shown in Fig. 20 demonstrate a dose dependent increase in the growth rate of bones treated with MS-PRO 59 in comparison to non-relevant control LY6.3 Fab. The LY6.3-treated control femurs, marked with a circle, grew at the slowest rate. The MSPRO59 treated femurs exhibited a higher growth rate, with the optimal rate achieved at MSPRO59

20   concentration of 100ug/ml (square) while the higher cocentration (400ug/ml, triangle) showed inhibition. Moreover, the growth rates achieved by 400 microgram/ml of MSPRO59 doubled in comparison to the control Ab (3.55 U/day as compared to 1.88 U/day, respectively). This experiment shows the neutralizing effect of the MSPRO59 antibody on constitutively active FGFR3, in an _ex vivo_ model.

25   **Example 14: _In-vivo_ trials**

FDCP-FR3ach cells, but not FDCP (control) cells, were found to be tumorigenic when injected into nude mice. Each of 9 mice received two sub-cutaneous injections with different amount of transfected cells. Fourteen days after injection, progressively growing tumors started to appear at the site of FDCP-FR3ach injection but not at the FDCP site of injection.

30   External examination of the tumors showed a high vascular capsule. [125]I-labeled MSPRO59 and LY6.3 were injected I.P. into nude mice carrying the FDCP-FR3ach derived tumor. The

tumors were dissected 4 and 24 hrs later and radioactivity was measured. Concentration of MSPRO59 Abs in FDCP-FR3ach derived tumors is shown in Fig. 22.

Example 15: Animal Model for Bladder Carcinoma

5   Recent studies have shown that the IIIb isoform of FGFR3 is the only form expressed in bladder carcinoma, in particular an FGFR3 with an amino acid substitution wherein Serine 249 is replaced by Cysteine (S249C). The progression of the cancer is believed to be a result of the constitutive activation resulting from this amino acid substitution. In order to create the FGFR3 IIIb form, we isolated the IIIb region of FGFR3 from HeLa cells and generated a full length FGFR3IIIb isoform in

10   pLXSN. Retroviruses, expressing either normal FGFR3 (FR3wt) or mutant FGFR3 (FR3-S249C) were produced and used to infect FDCP cells. Stable pools were generated and further used for *in-vitro* and *in-vivo* experiments.

A. MSPRO59 reduces tumor size in mice

Twelve nude mice were injected with $2x10^6$ FDCP-S249C cells subcutaneous at 2 locations, one on

15   each flank. A week later MSPRO59 was administered i.p. at 400ug per mouse (3 mice in total), followed by 3 injections of 275 ug each, in 2 to 3 days intervals. Following 24 and 26 days the tumor size was measures. Figure 23 shows the inhibitory effect of MSPRO59 on tumor size.

B. Treating FDCP-S249C-derived tumors with MSPRO59

Nude mice (3 in each group), were injected subcutaneous at 2 locations, one on each flank,

20   with $2x10^6$ FDCP-S249C cells each. A week later, 400 or 80 μg MSPRO59 were injected IP. Three days later, mice were injected with 400 μg followed by 5 additional injections with 275 μg MSPRO59, each, every 3 or 4 days. Mice initially treated with 80 μg MSPRO59 were similarly given an additional 80 μg MSPRO59 followed by 5 injections with 50 μg MSPRO59 at the same schedule. Mice injected with PBS were used as control. Tumors

25   typically appeared three weeks post injection of the cells. Tumor volume was estimated from measurements in 3 dimensions at 16,20, 23 or 32 days post cell injection.

As shown in Figure 24 there is both a delay in tumor appearance and an inhibitory effect on tumor progression in the treated mice. This indicates that these FGFR3 inhibitors are potent *in-vivo*.

30   These data may also help us understand the mechanism by which the S249C-derived tumors were developed. Since we are using pools of cells, treatment with MSPRO59 inhibited the

susceptible cells, leading to delay in tumor appearance. However, over time, the resistant cells survived and proliferated, giving rise to a solid tumor.

C. MSPRO59 inhibits FDCP-FR3ach380 derived tumor growth.

Nude mice were injected subcutaneously in the flank with $2x10^6$ FDCP-FR3ach380 cells, each. Treatment with MSPRO59 began at the day of tumor appearance. Three mice were treated with a known tyrosine kinase inhibitor (TKI -50 mg/Kg/injection) and three with 400 µg followed by 3 additional injections with 300 µg MSPRO59, every 3 or 4 days. Three mice were treated with PBS alone as control. The tumor size was estimated as before at the indicated days after cell injection. The dose schedule is shown in Table 7 below.

Table 7

	Days After FDCP-FR3^{ach380} Cell Injection			
	21	25	28	31
MSPRO59 (µg)	400µg	300µg	300µg	300µg
PBS (µl)	50	50	50	50

Results are shown in bar graph format in Figure 25A.

D. MSPRO59 inhibits FDCP-S249C induced tumor growth

To overcome the instability of the FDCP-derived pools, clones from each pool FDCP-S249C clone #2) were isolated and characterized. These clones were tested in an XTT proliferation assay and were shown to be inhibited by MSPRO59. $2x10^6$ cells from each clone were injected into nude mice. Tumors appeared 18-30 after injection.

FDCP-S249C clone #2 was injected subcutaneously on the flank. A week later mice were injected with 280 µg MSPRO59 single chain (SC) I.P. every day. Mice injected with PBS were used as control. Tumor volume was estimated from measurements in 3 dimensions at 18 or 24 days post cell injection. An apparent inhibition of tumor growth by MSPRO59(SC) was observed in tumors derived from clone 2 (figure 26). Figure 25B shows the inhibition effected by MSPRO59scFv and MSPRO59 Fab compared to the control. Both inhibit growth of the tumor resulting from constitutively activated cells.

Having now fully described this invention, it will be appreciated by those skilled in the art that the same can be performed within a wide range of equivalent parameters, concentrations, and conditions without departing from the spirit and scope of the invention and without undue experimentation.

While this invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications. This application is intended to cover any variations, uses, or adaptations of the inventions following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth as follows in the scope of the appended claims.

All references cited herein, including journal articles or abstracts, published or corresponding U.S. or foreign patent applications, issued U.S. or foreign patents, or any other references, are entirely incorporated by reference herein, including all data, tables, figures, and text presented in the cited references. Additionally, the entire contents of the references cited within the references cited herein are also entirely incorporated by references.

Reference to known method steps, conventional methods steps, known methods or conventional methods is not in any way an admission that any aspect, description or embodiment of the present invention is disclosed, taught or suggested in the relevant art.

The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art (including the contents of the references cited herein), readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance presented herein, in combination with the knowledge of one of ordinary skill in the art.

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CLAIMS

1. A molecule comprising the antigen binding portion of an isolated antibody which has specific binding affinity for a receptor protein tyrosine kinase and which blocks constitutive activation of said receptor protein tyrosine kinase.

2. The molecule according to claim 1, wherein said molecule binds to the extracellular domain of the receptor protein tyrosine kinase.

3. The molecule according to claim 1 wherein the antibody binds the dimeric form of the receptor.

4. The molecule according to claim 1, wherein the receptor protein tyrosine kinase is selected from the group consisting of EGFR/ErbB1, ErbB2/HER2/Neu, ErbB/HER3, ErbB4/HER4, IGF-1R, PDGFR-α, PDGFR-β, CSF-1R, kit/SCFR, Flk2/FH3, Flk1/VEGFR1, Flk1/VEGFR2, Flt4/VEGFR3, FGFR1, FGFR2/K-SAM, FGFR3, FGFR4, TrkA, TrkC, HGFR, RON, EphA2, EphB2, EphB4, Axl, TIE/TIE1, Tek/TIE2, Ret, ROS, Alk, Ryk, DDR, LTK and MUSK, and heterodimeric combinations thereof.

5. The molecule according to claim 4, wherein said receptor protein tyrosine kinase is a fibroblast growth factor receptor (FGFR).

6. The molecule according to claim 5, wherein said FGFR is FGFR3.

7. A pharmaceutical composition, comprising, as an active ingredient, the molecule according to any one of claims 1 through 6 and a pharmaceutically acceptable carrier, excipient, or auxiliary agent.

8. A molecule comprising the antigen-binding portion of an antibody which has specific binding affinity for a fibroblast growth factor receptor (FGFR) and which blocks ligand-dependent activation of said FGFR.

9. The molecule according to claim 8, wherein said molecule binds to the extracellular domain of the FGFR.

10. The molecule according to claim 9, wherein the FGFR is FGFR3.

11. A pharmaceutical composition, comprising the molecule according to any one of claims 8-10 and a pharmaceutically acceptable carrier, excipient, or auxiliary agent.

12. A kit comprising a molecule of any one of claims 1-6 and 8-10 and at least one reagent suitable for detecting the presence of said molecule when bound to said receptor protein tyrosine kinase and instructions for use.

13. A method for treatment of bone and cartilage related disorders, comprising administering a therapeutically effective amount of the pharmaceutical composition according to claim 7 or 11 to a subject in need thereof.

14. The method according to claim 13 wherein the skeletal disorder is a skeletal dysplasia or a craniosynostosis disorder.

15. The method according to claim 14 wherein said craniosynostosis disorder is Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis nigricans.

16. The method according to claim 13 wherein the skeletal dysplasia is selected from achondroplasia, thanatophoric dysplasia (TD), hypochondroplasia, severe achondroplasia with developmental delay and acanthosis nigricans (SADDAN) dysplasia.

17. The method according to claim 16, wherein the skeletal dysplasia is achondroplasia.

18. The method according to claim 13 for treating or inhibiting a malignant cell proliferative disease or disorder associated with abnormal RPTK activity.

19. The method according to claim 18 wherein the malignant cell proliferative disease or disorder is a hematopoietic malignancy.

20. The method according to claim 19 wherein the hematopoietic malignancy is multiple myeloma.

21. The method according to claim 18 for the treatment or inhibition of solid tumors.

22. The method according to claim 21 wherein the solid tumors are selected from mammary, colon, cervical, bladder, colorectal, chondrosarcoma or osteosarcoma.

23. The method according to claim 18 for treating or inhibiting tumor formation, primary tumors, tumor progression or tumor metastasis.

24. The method according to claim 23 wherein tumor progression is the progression of transitional cell carcinoma.

25. The method according to claim 19 wherein the disorder is associated with the action of a constitutively activated receptor protein tyrosine kinase, and wherein the administered pharmaceutical composition is the pharmaceutical composition according to claim 7.

26. The method according to claim 19, wherein the disorder is associated with ligand-dependent activation of a receptor protein tyrosine kinase, and wherein the administered pharmaceutical composition is the pharmaceutical composition according to claim 11.

27. The method according to claim 18 for treatment of hyperproliferative diseases and disorders associated with ligand dependent fibroblast growth factor receptor signaling.

28. The method according to claim 27 wherein the hyperproliferative diseases and disorders are vision disorders such as neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy.

29. The method according to claim 27 wherein the hyperproliferative diseases are non-neoplastic angiogenic pathologic conditions such as hemangiomas, angiofibromas and psoriasis

30. The method according to claim 18, wherein the disorder is associated with constitutive activation of a receptor protein tyrosine kinase, and wherein the administered pharmaceutical composition is the pharmaceutical composition according to claim 7.

31. The method according to claim 18, wherein the disorder is associated with ligand-dependent activation of a receptor protein tyrosine kinase, and wherein the administered pharmaceutical composition is the pharmaceutical composition according to claim 11.

32. A method for treating or inhibiting a cell proliferative disease or disorder, comprising administering a therapeutically effective amount of the pharmaceutical composition according to claim 7 or 11 to a subject in need thereof.

33. The method according to claim 19, wherein the cell proliferative disease or disorder is tumor progression.

34. The method according to claim 20, wherein the tumor progression is the progression of transitional cell carcinoma.

35. The method according to claim 20, wherein the tumor progression is the progression of osteo or chondrosarcoma.

36. The method according to claim 20, wherein the tumor progression is the progression of multiple myeloma.

37. The method according to claim 19 wherein the receptor protein tyrosine kinase is FGFR3 and the tumor progression is the progression of mammary carcinoma.

38. A method for screening a molecule comprising the antigen-binding portion of an antibody which blocks ligand-dependent activation of a receptor protein tyrosine kinase, comprising:

screening a library of antibody fragments for binding to a dimeric form of a receptor protein tyrosine kinase;

identifying an antibody fragment which binds to the dimeric form of the receptor protein tyrosine kinase as a candidate molecule for blocking ligand-dependent activation of the receptor protein tyrosine kinase;

and determining whether or not the candidate molecule can block ligand-dependent activation of the receptor protein tyrosine kinase in a cell.

39. The method according to claim 38, wherein the receptor protein tyrosine kinase is a fibroblast growth factor receptor

40. The method according to claim 39, wherein the fibroblast growth factor receptor is FGFR3.

41. A molecule according to claim 1 comprising V_H-CDR3 and V_L-CDR3 regions, selected from the group consisting of SEQ ID NO: 8 and 9; SEQ ID NO: 12 and 13; and SEQ ID NO: 24 and 25.

42. The molecule according to claim 41, comprising V_L region and V_H regions, selected from the group consisting of SEQ ID NO: 92 and 103; SEQ ID NO: 94 and 105 and SEQ ID NO: 102 and 113.

43. A pharmaceutical composition, comprising, as an active ingredient, the molecule according to any one of claims 41 or 42 and a pharmaceutically acceptable carrier, excipient, or auxiliary agent.

44. An isolated nucleic acid molecule, comprising a sequence selected from SEQ ID NO: 30, 31, 34, 35, 50 or 51 or a nucleotide sequence hybridizing under high stringency conditions thereto.

45. An isolated nucleic acid molecule, comprising a sequence selected from SEQ ID NO: 74, 75, 76, 84, 89 or 91 and 87or a nucleotide sequence hybridizing under high stringency conditions thereto.

46. The isolated nucleic acid molecule of claim 44, comprising nucleotides encoding a V_L-CDR3 DNA region and a V_H-CDR3 DNA region, respectively, selected from the group consisting of SEQ ID NO: 30 and 31; SEQ ID NO:34 and 35; SEQ ID NO: 50 and 51.

47. The isolated nucleic acid molecule of claim 45 comprising nucleotides encoding a V_L region and a V_H region, respectively, selected from the group consisting of SEQ ID NO: 74 and 84 ; SEQ ID NO:75 and 89; and SEQ ID NO: 76 and 91.

48. A vector comprising a nucleic acid molecule according to claim 46 or 47.

49. The vector according to claim 48 wherein the vector is an expression vector.

50. The host cell transformed with the vector according to claim 48 or 49.

51. A molecule according to claim 8 comprising the combination of V_H-CDR3 and V_L-CDR3 amino acid sequences selected from the group consisting of SEQ ID NO:10 and SEQ ID NO:11; SEQ ID NO:14 and SEQ ID NO:15; SEQ ID NO:16 and SEQ ID NO:17; SEQ ID NO:18 and SEQ ID NO:19; SEQ ID NO:20 and SEQ ID NO:21; SEQ ID NO:22 and SEQ ID NO:23, SEQ ID NO:26 and SEQ ID NO:27 or SEQ ID NO:28 and SEQ ID NO:29.

52. The molecule according to claim 51, comprising a V_L region and a V_H region, respectively, selected from the group consisting of respectively, selected from the group consisting of SEQ ID NO: 92 and 103; SEQ ID NO: 93 and 104; SEQ ID NO: 94 and 105; SEQ ID NO:95 and 106; SEQ ID NO: 96 and 107 ; SEQ ID NO: 97 and 108; SEQ ID NO:98 and 109; SEQ ID NO: 99 and 110; SEQ ID NO: 100 and 111; SEQ ID NO: 101 and 112; and SEQ ID NO:102 and 113.

53. A pharmaceutical composition, comprising the molecule according to any one of claims 51-52 and a pharmaceutically acceptable carrier, excipient, or auxiliary agent.

54. An isolated nucleic acid molecule, comprising SEQ ID NO: NO:32, 33, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 48, and 49 or a nucleotide sequence hybridizing under high stringency conditions thereto.

55. An isolated nucleic acid molecule, comprising SEQ ID NO: 62, 64, 65, 67, 69, 70, 76, 78, 79, 80, 83, 85, 86, and 87or a nucleotide sequence hybridizing under high stringency conditions thereto.

56. An isolated nucleic acid molecule, comprising nucleotides encoding a V_L-CDR3 DNA region and a V_H-CDR3 DNA region, respectively, selected from the group consisting of SEQ ID NO: 32 and 33; SEQ ID NO:36 and 37; SEQ ID NO: 38 and 39, SEQ ID NO:40 and 41, SEQ ID NO: 42 and 43, SEQ ID NO: 44 and 45, SEQ ID NO: 48 and 49.

57. An isolated nucleic acid molecule, comprising nucleotides encoding a V_L region and a V_H region, respectively, selected from the group consisting of SEQ ID NO: 70 and 85; SEQ ID NO:67 and 78; SEQ ID NO:64 and 79; SEQ ID NO:71 and 86; SEQ ID NO:62 and 80; SEQ ID NO:65 and 87; SEQ ID NO:69 and 83.

58. A vector comprising a nucleic acid molecule according to claim 56 or 57.

59. The vector according to claim 58 which is an expression vector.

60. The host cell transformed with the vector according claim 58 or 59.

61. A method for treatment of bone and cartilage related disorders, comprising administering a therapeutically effective amount of the pharmaceutical composition according to claim 43 or 53 to a subject in need thereof.

62. The method according to claim 61 wherein the skeletal disorder is a skeletal dysplasia or a craniosynostosis disorder.

63. The method according to claim 62 wherein said craniosynostosis disorder is Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis nigricans.

64. The method according to claim 63 wherein the skeletal dysplasia is selected from achondroplasia, thanatophoric dysplasia (TD), hypochondroplasia, severe achondroplasia with developmental delay and acanthosis nigricans (SADDAN) dysplasia.

65. The method according to claim 64, wherein the skeletal dysplasia is achondroplasia.

66. The method according to claim 61 for treating or inhibiting a malignant cell proliferative disease or disorder associated with abnormal RPTK activity.

67. The method according to claim 66 wherein the malignant cell proliferative disease or disorder is a hematopoietic malignancy.

68. The method according to claim 67 wherein the hematopoietic malignancy is multiple myeloma.

69. The method according to claim 61 for the treatment or inhibition of solid tumors.

70. The method according to claim 69 wherein the solid tumors are selected from mammary, colon, cervical, bladder, colorectal, chondrosarcoma or osteosarcoma.

71. The method according to claim 61 for treating or inhibiting tumor formation, primary tumors, tumor progression or tumor metastasis.

72. The method according to claim 71 wherein tumor progression is the progression of transitional cell carcinoma.

73. The method according to claim 61 wherein the disorder is associated with the action of a constitutively activated receptor protein tyrosine kinase, and wherein the administered pharmaceutical composition is the pharmaceutical composition according to claim 43.

74. The method according to claim 61, wherein the disorder is associated with ligand-dependent activation of a receptor protein tyrosine kinase, and wherein the administered pharmaceutical composition is the pharmaceutical composition according to claim 53.

75. The method according to claim 74 for treatment of hyperproliferative diseases and disorders associated with ligand dependent fibroblast growth factor receptor signaling.

76. The method according to claim 75 wherein the hyperproliferative diseases and disorders are vision disorders such as neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy.

77. The method according to claim 75 wherein the hyperproliferative diseases are non-neoplastic angiogenic pathologic conditions such as hemangiomas, angiofibromas and psoriasis

78. The method according to claim 73, wherein the disorder is associated with constitutive activation of a receptor protein tyrosine kinase, and wherein the administered pharmaceutical composition is the pharmaceutical composition according to claim 43.

79. The method according to claim 74, wherein the disorder is associated with ligand-dependent activation of a receptor protein tyrosine kinase, and wherein the administered pharmaceutical composition is the pharmaceutical composition according to claim 53.

80. A method for treating or inhibiting a cell proliferative disease or disorder, comprising administering a therapeutically effective amount of the pharmaceutical composition according to claim 43 or 53 to a subject in need thereof.

81. The method according to claim 80, wherein the cell proliferative disease or disorder is tumor progression.

82. The method according to claim 81, wherein the tumor progression is the progression of transitional cell carcinoma.

83. The method according to claim 81, wherein the tumor progression is the progression of osteo or chondrosarcoma.

84. The method according to claim 81, wherein the tumor progression is the progression of multiple myeloma.

85. The method according to claim 81 wherein the receptor protein tyrosine kinase is FGFR3 and the tumor progression is the progression of mammary carcinoma.
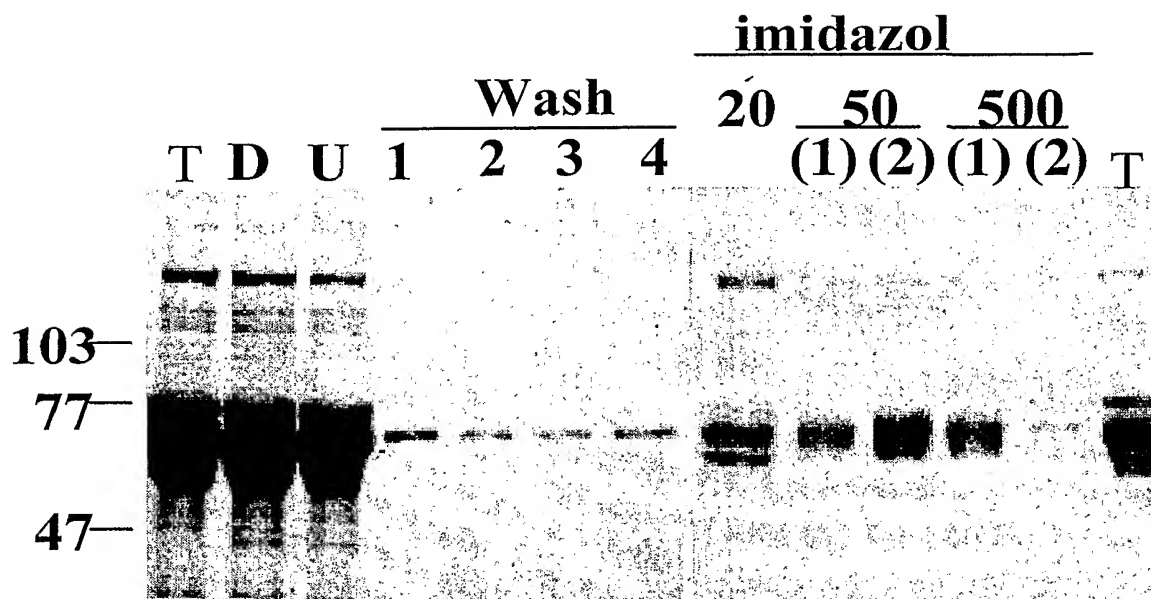
Figure 1

Figure 2
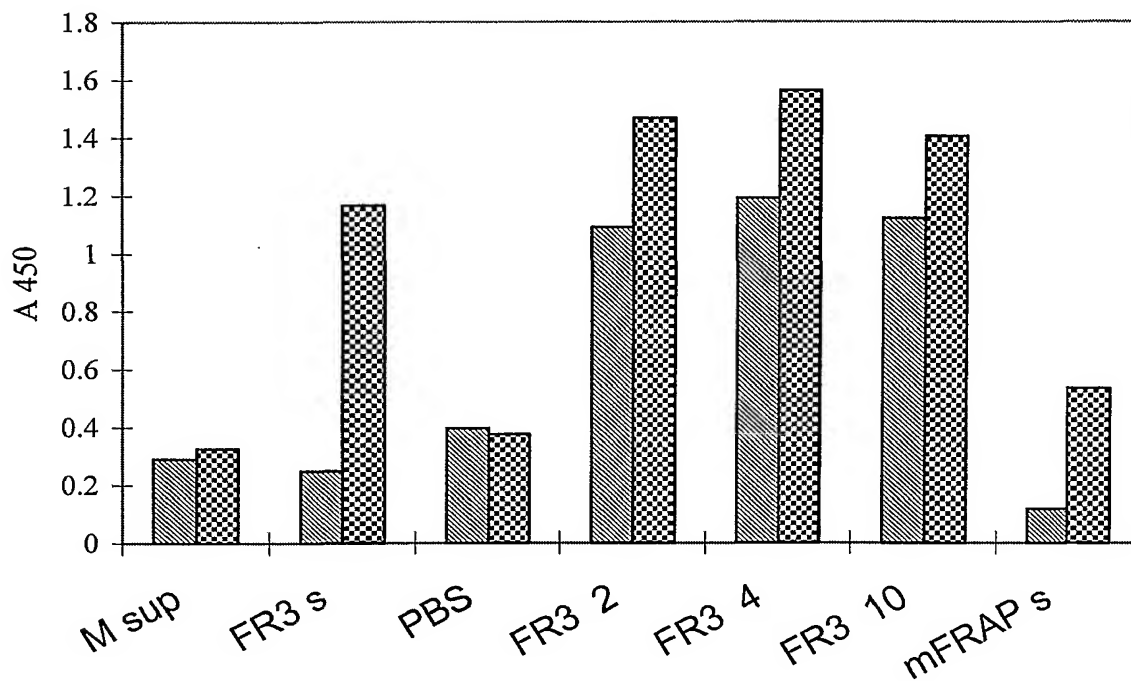
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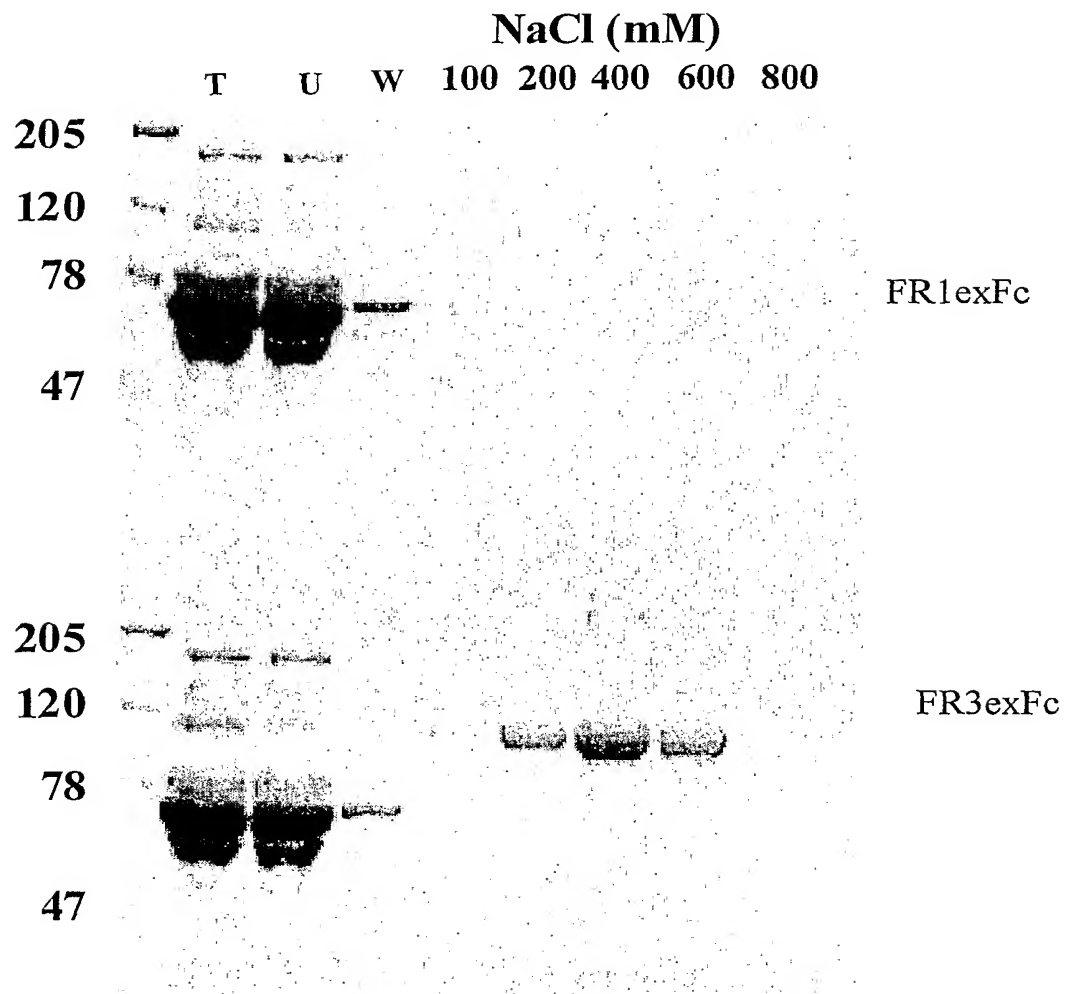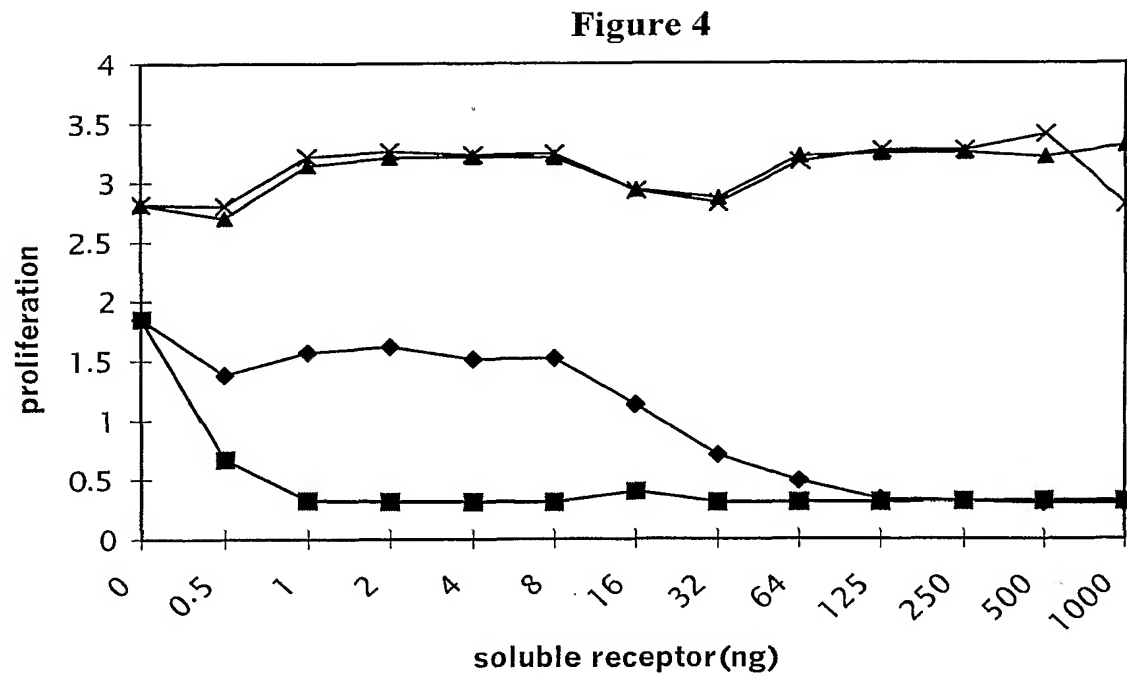
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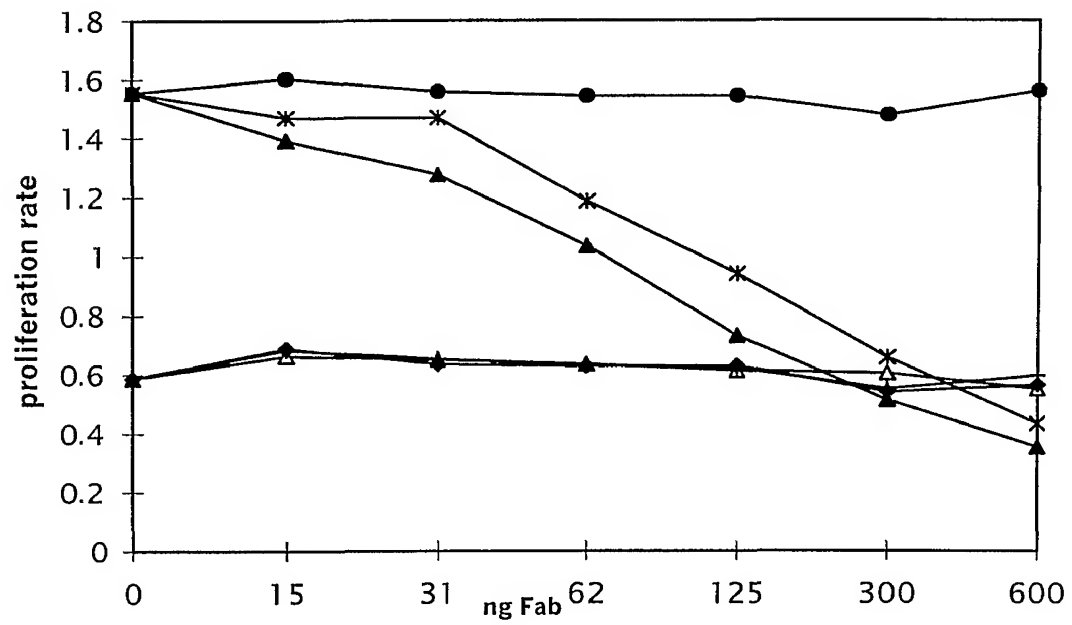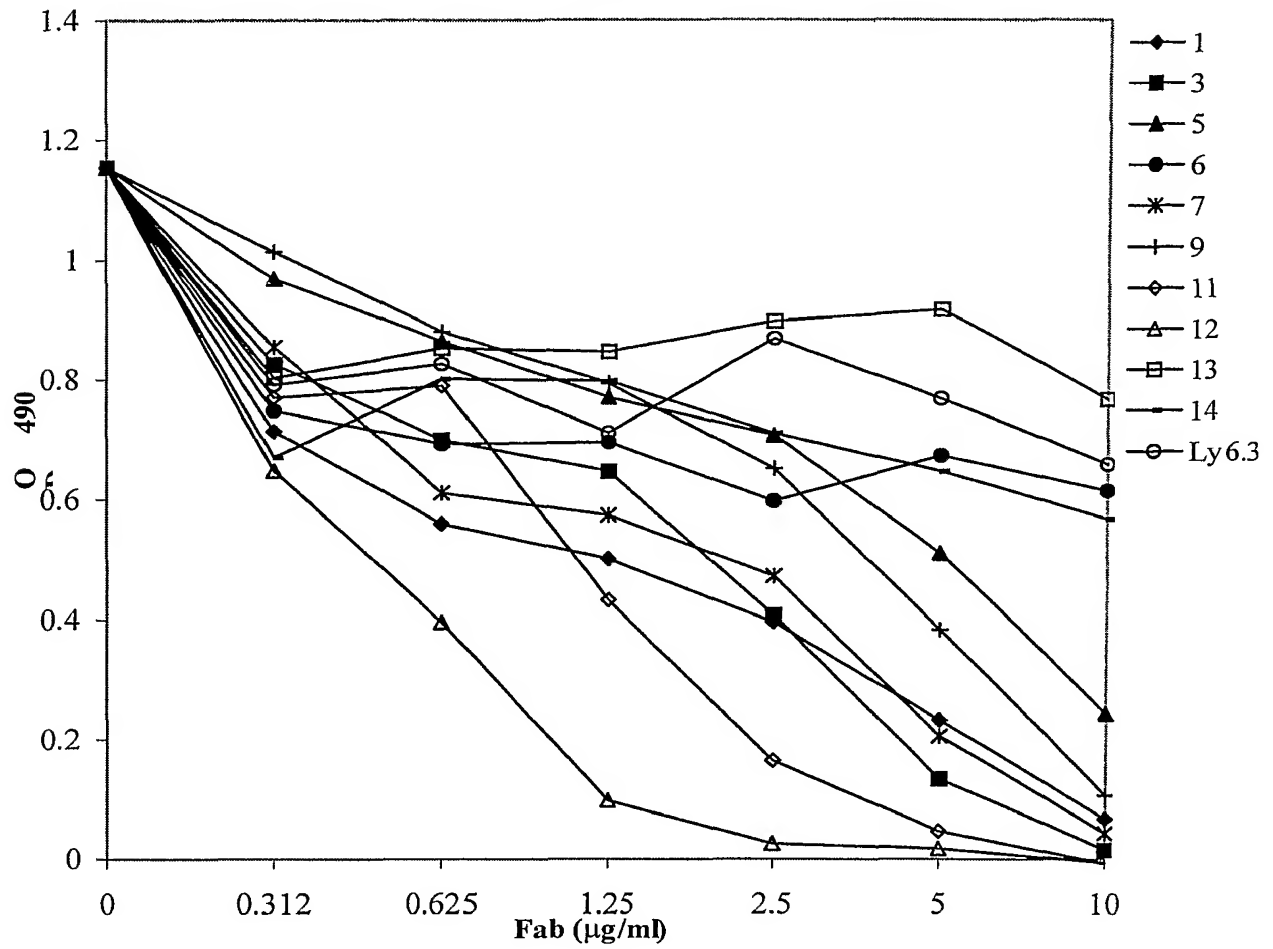
Figure 5

Figure 6

Figure 7A
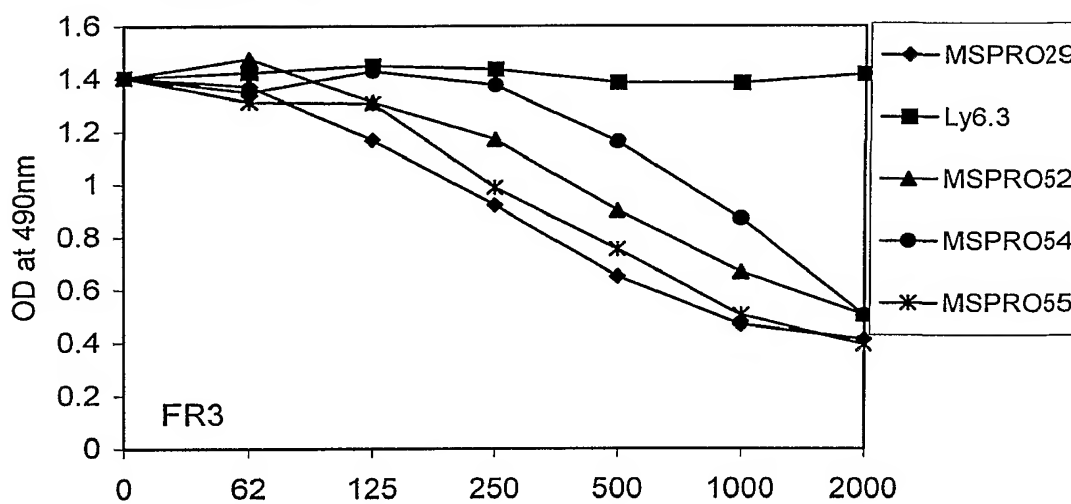
Figure 7B
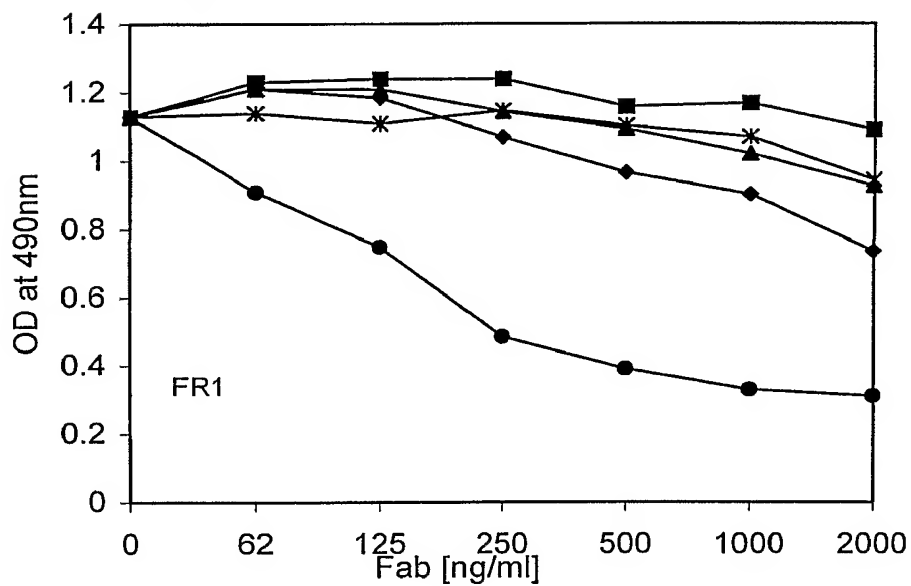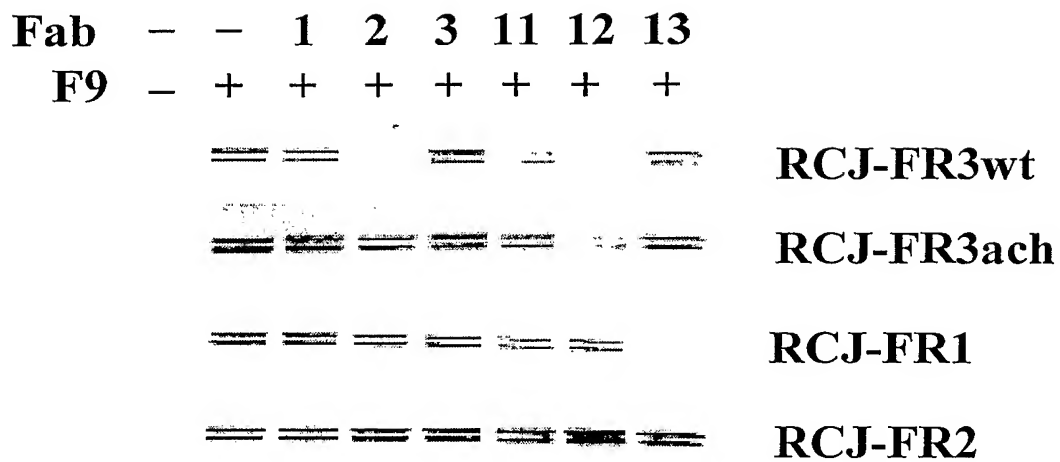
7/50

Figure 8A

Fab	–	–	1	2	3	11	12	13
F9	–	+	+	+	+	+	+	+

RCJ-FR3wt

RCJ-FR3ach

RCJ-FR1

RCJ-FR2

Figure 8B

			12				29				13			
Fab(μg)	—	—	1	5	20	50	1	5	20	50	1	5	20	50
F9	—	+	+	+	+	+	+	+	+	+	+	+	+	+

P-JNK

FIGURE 9A
<u>M14</u>

MSPRO (μg)
F9

FIGURE 9B
<u>W11</u>

MSPRO (μg)
F9

FIGURE 9C
<u>R1-1</u>

MSPRO (μg)
F9

FIGURE 9D
<u>R2-2</u>

MSPRO (μg)
F9

9/50

Figure 10

D1-3 ⎯⎯⎯⎯⎯⎯⎯⎯⎯⎯⎯⎯······················

D2-3 　　　　⎯⎯⎯⎯⎯⎯⎯⎯······················

D2 　　　　　⎯⎯⎯⎯⎯·····················

SP   Ig   AB   IgI   IgII   TM   Kinase

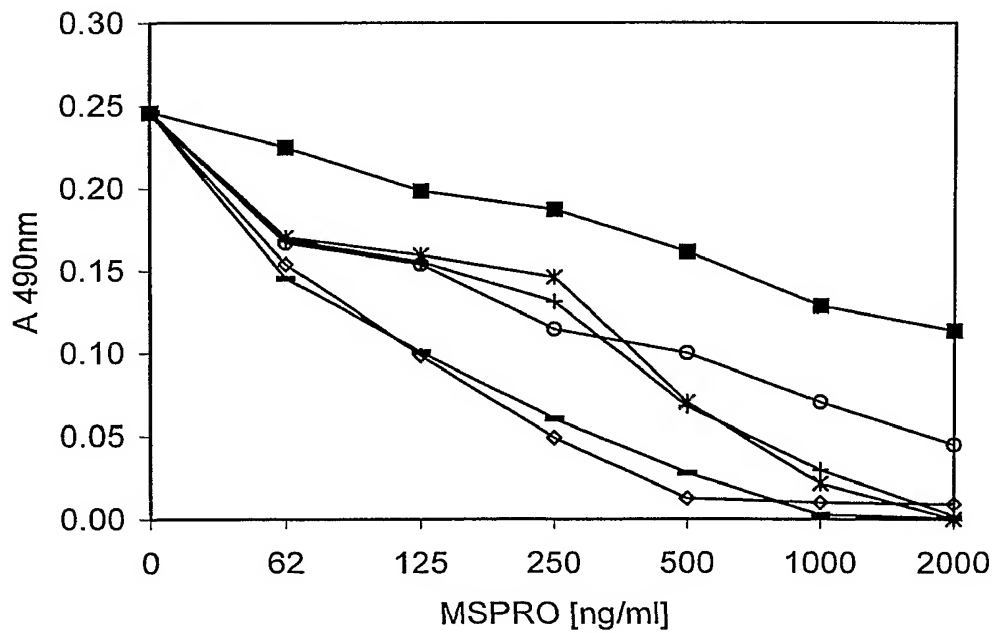1 19　61　109　133 143　176　228　275　339　372 396　472　573　589　748　800

Figure 11

11/50
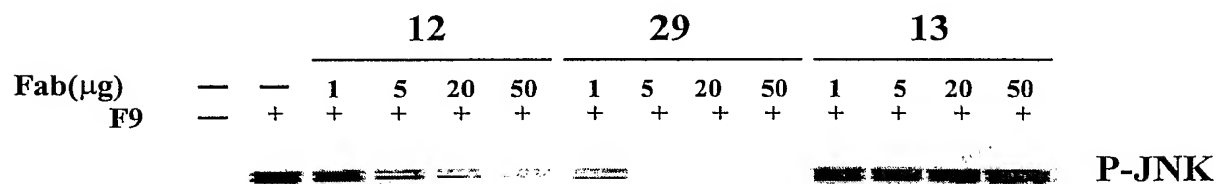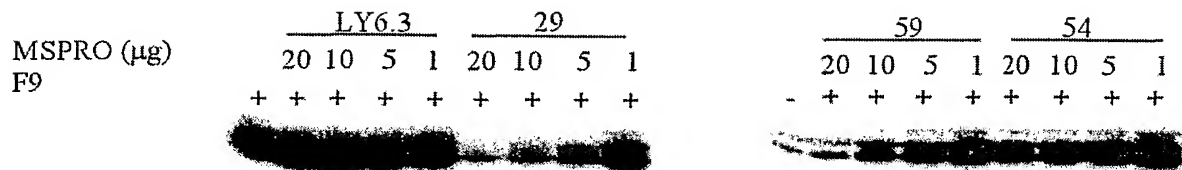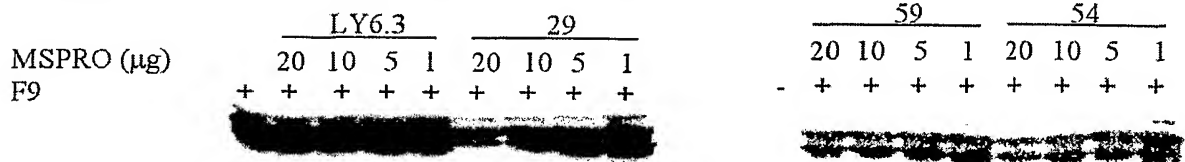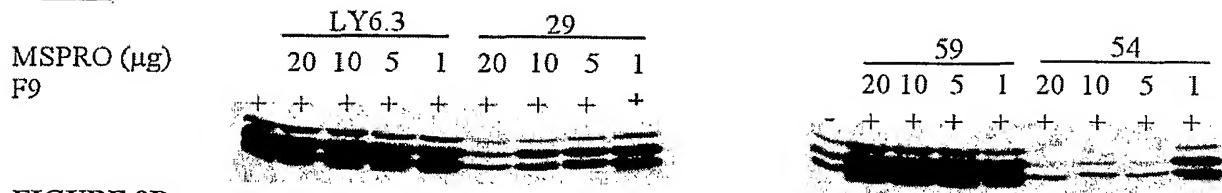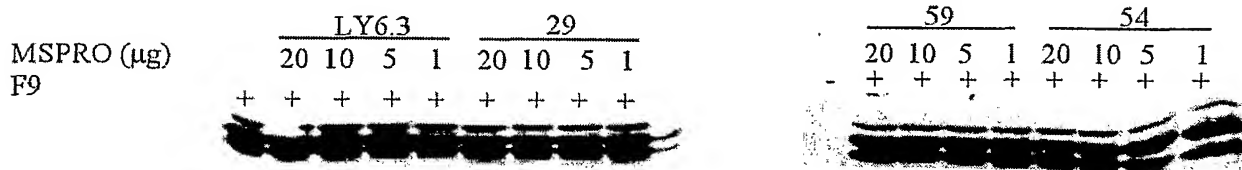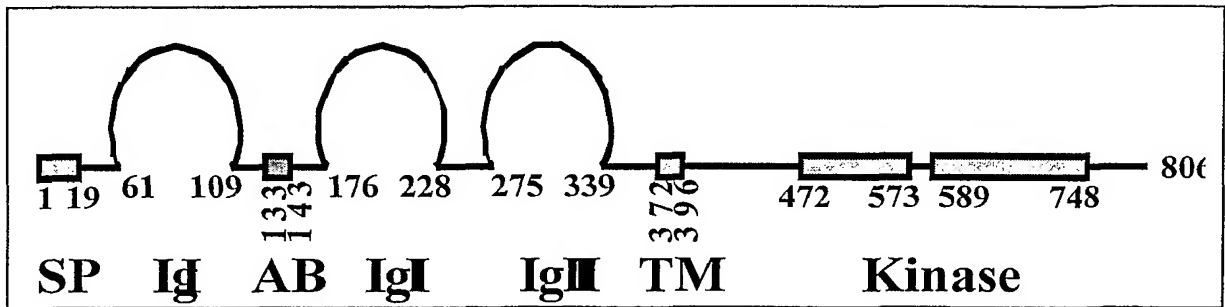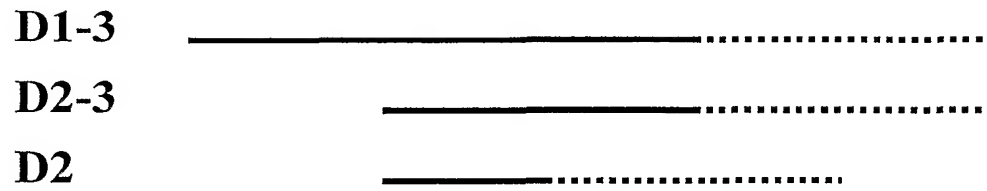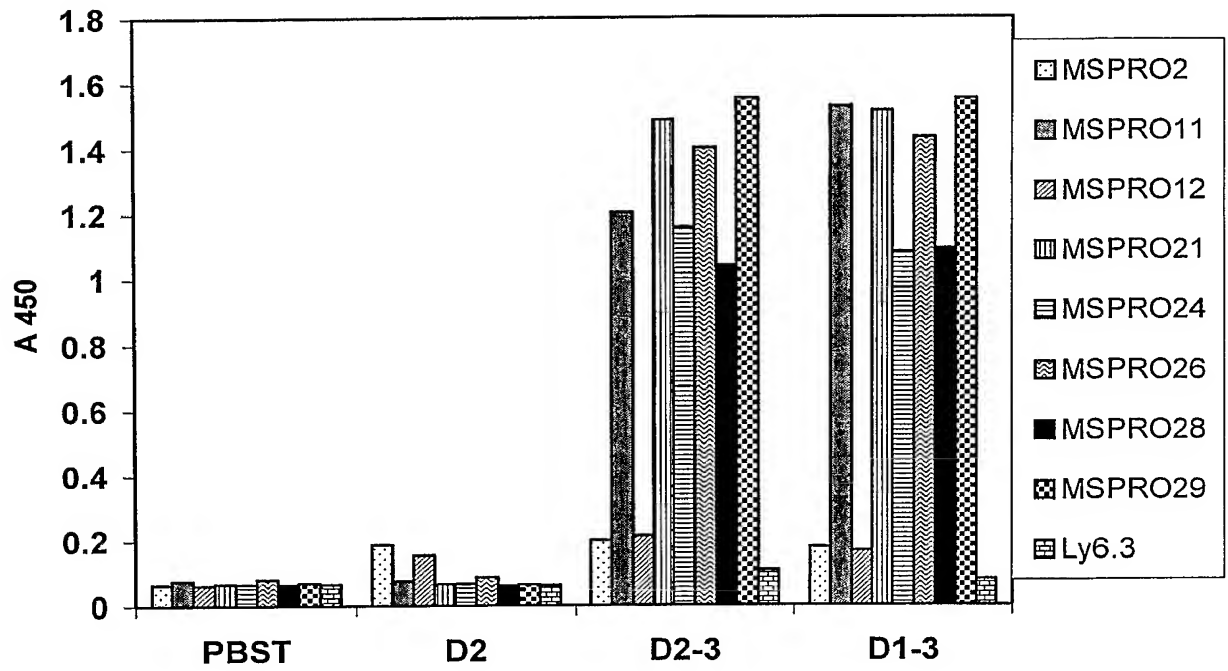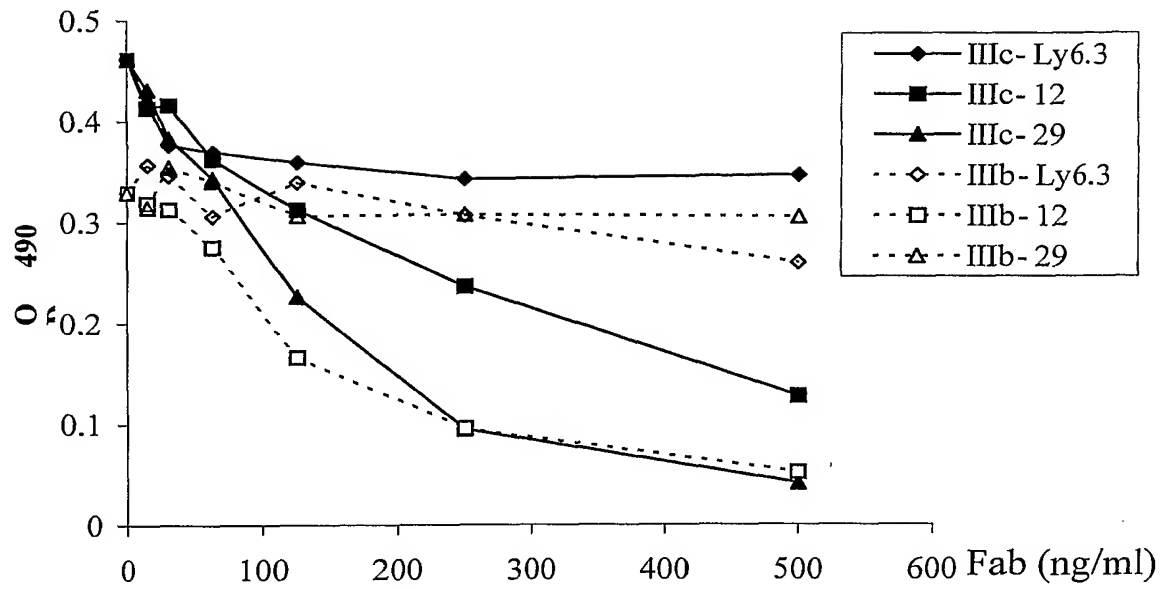
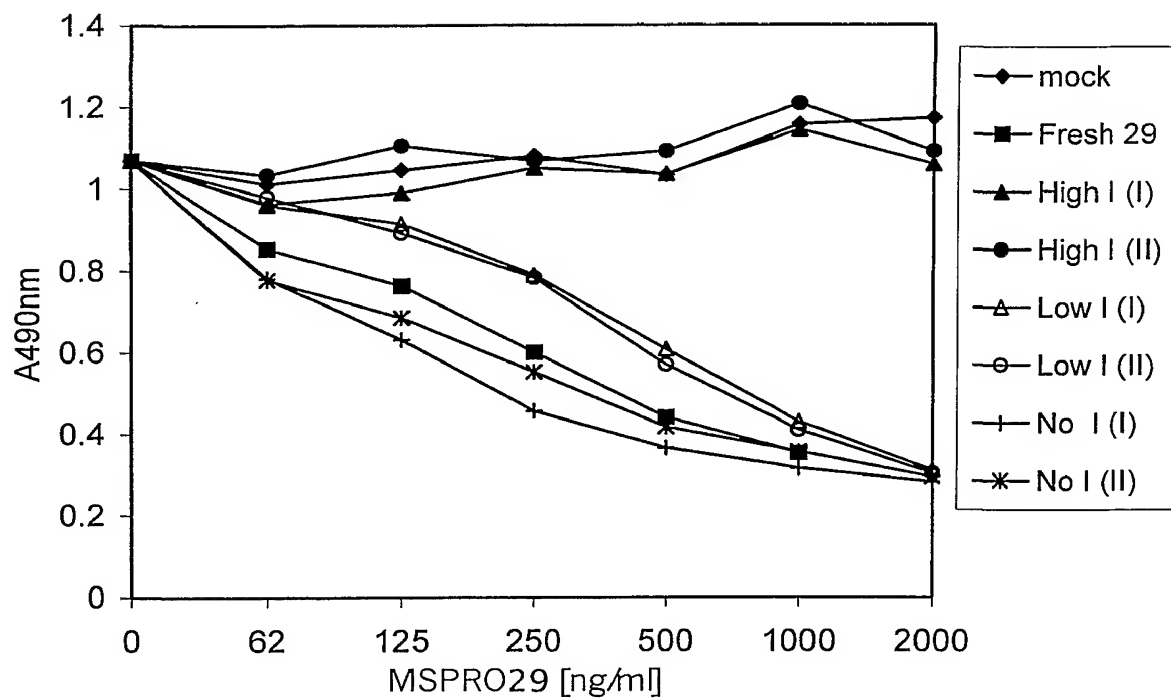Figure 12
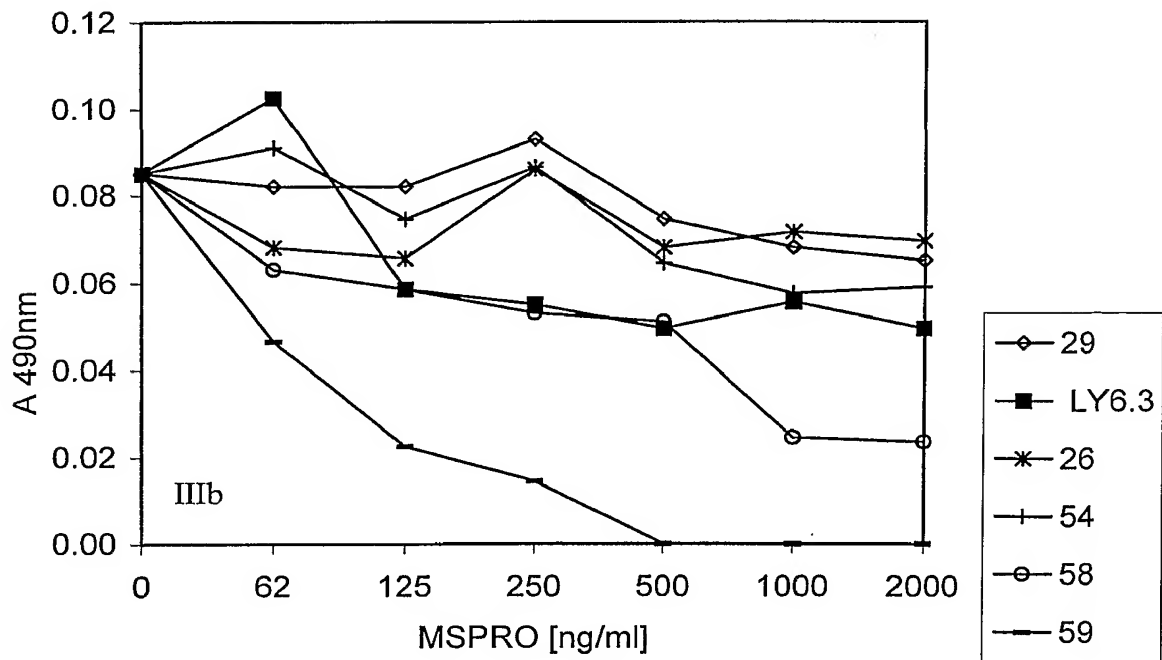
Figure 13A

Figure 13B

Figure 14
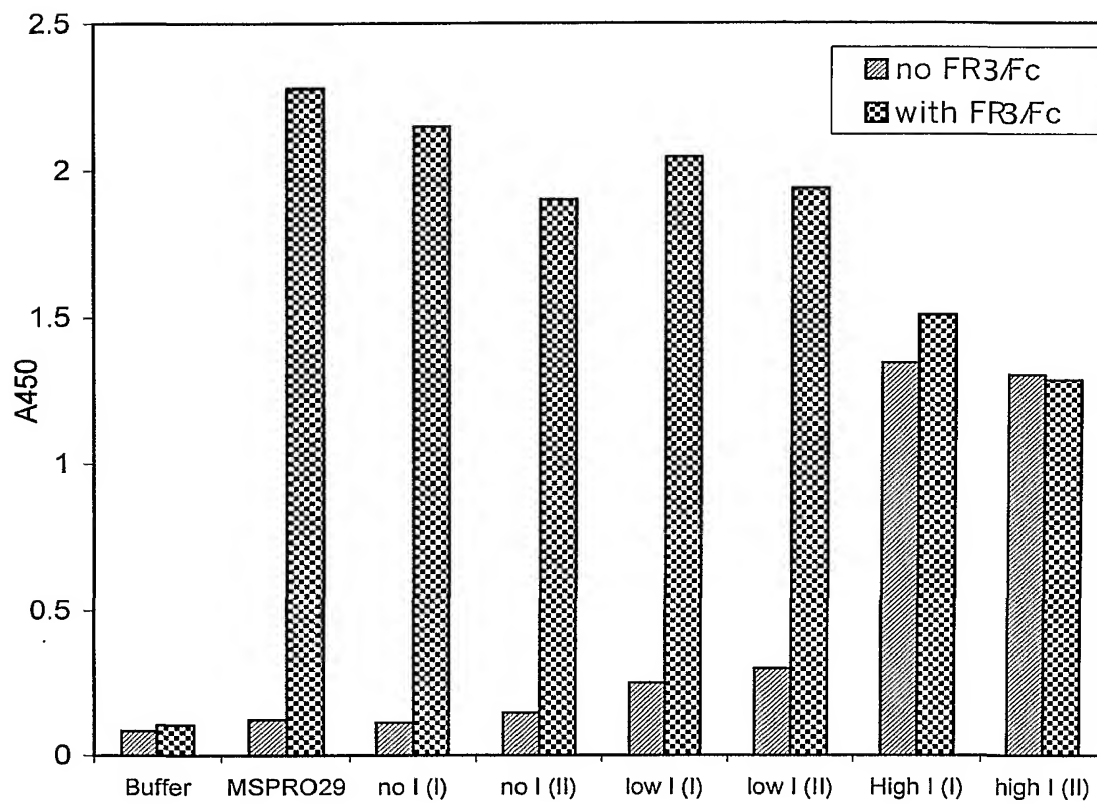
Figure 15

Figure 16
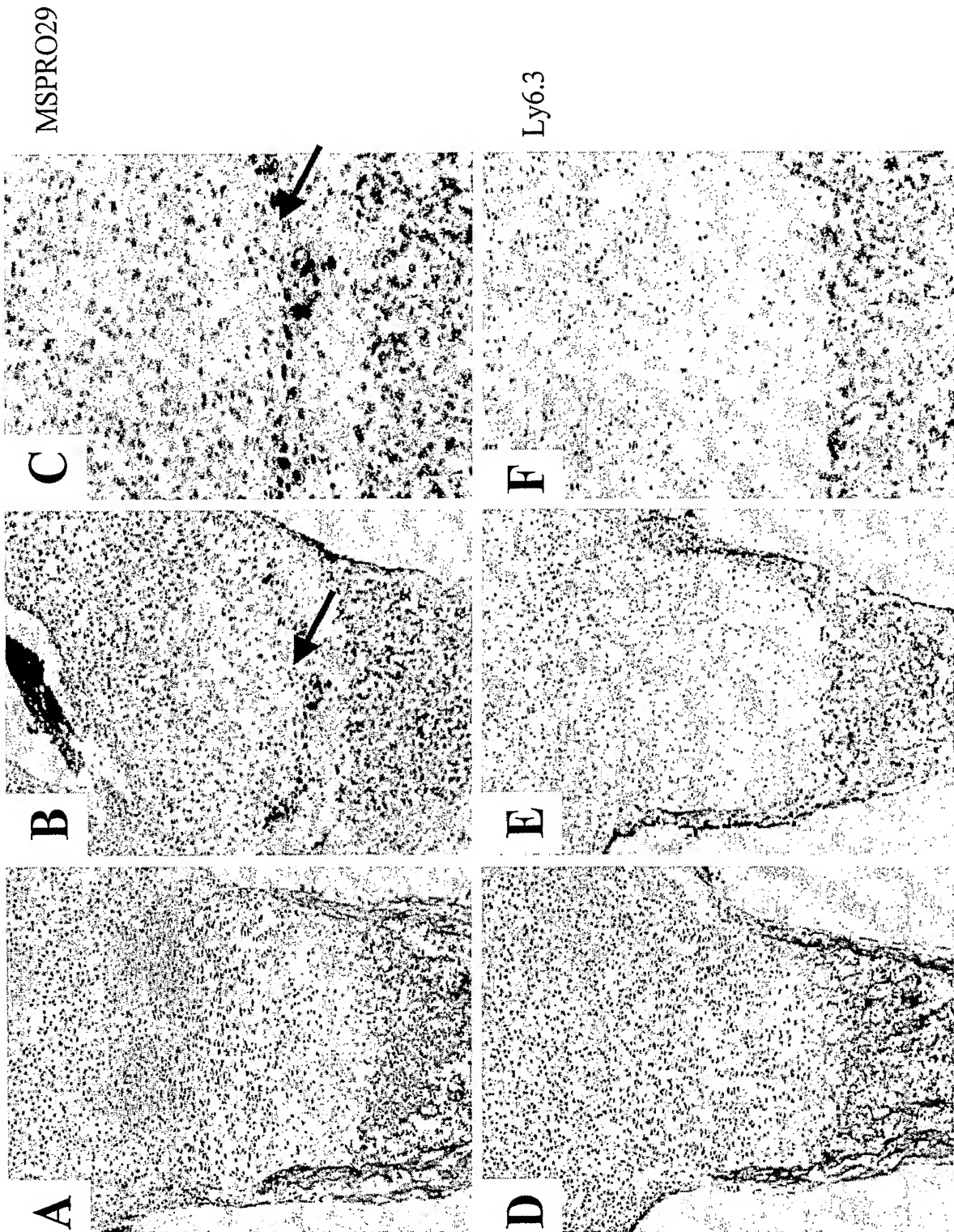
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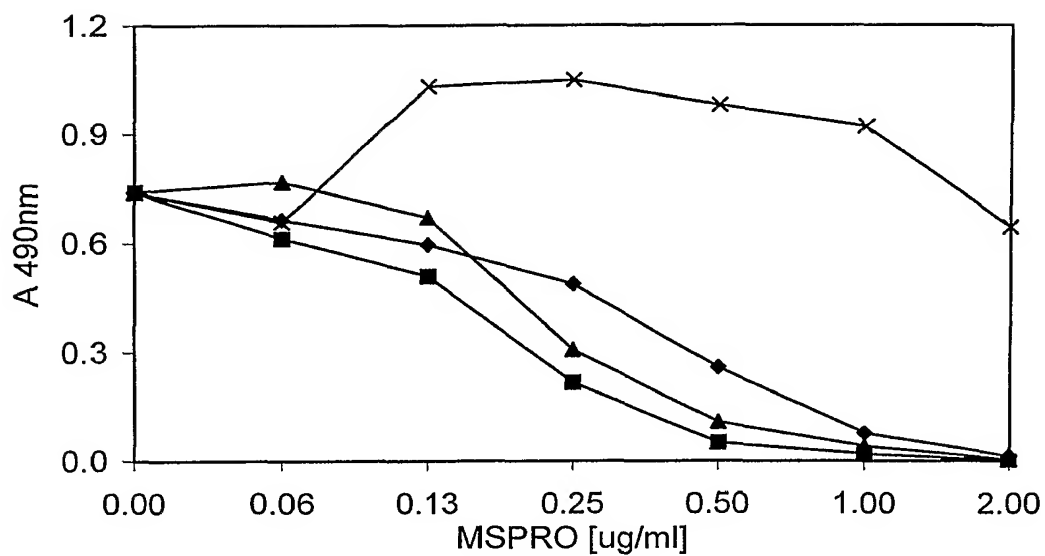
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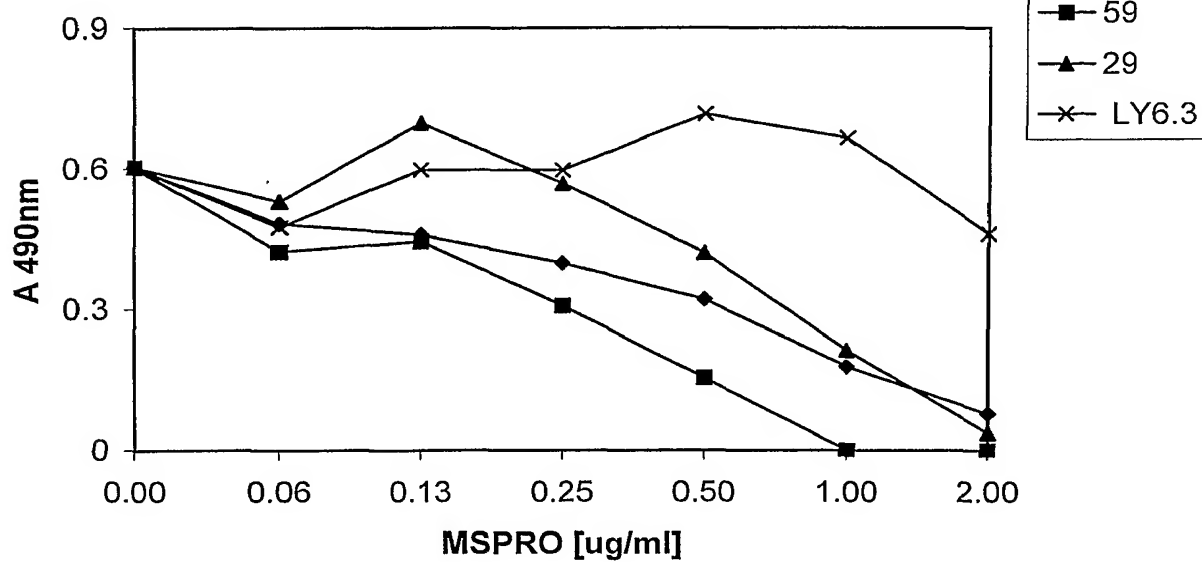
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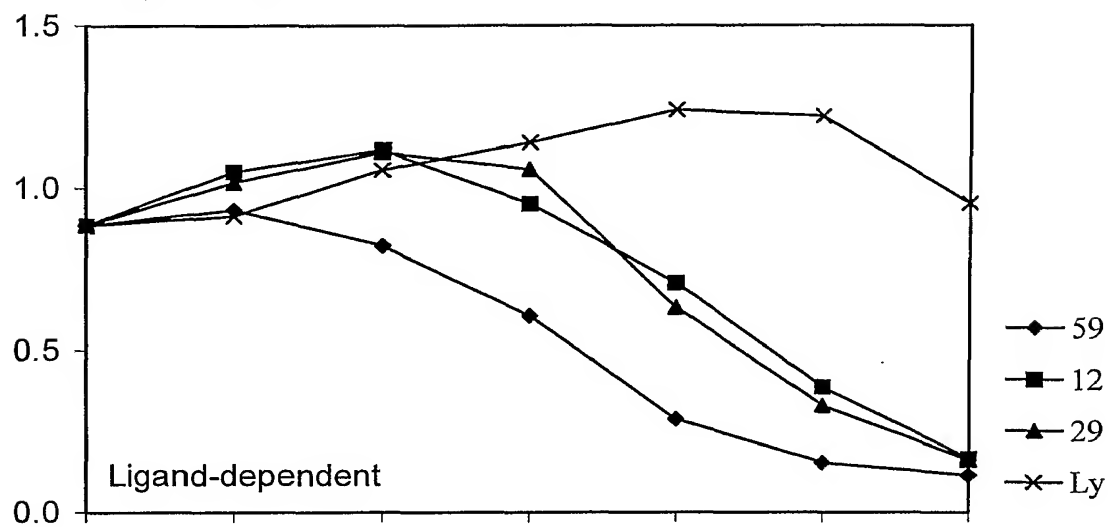
Figure 18B

Figure 19

Figure 20

Seed cells
↓
Remove tetracycline
↓
Serum starvation
↓
FGF9 stimulation
↓
Cell lysis

Immunoprecipitation with anti FGFR3
↓

SDS-PAGE/immunoblot with   SDS-PAGE/immunoblot with
anti active MAPK   anti phosphotyrosine
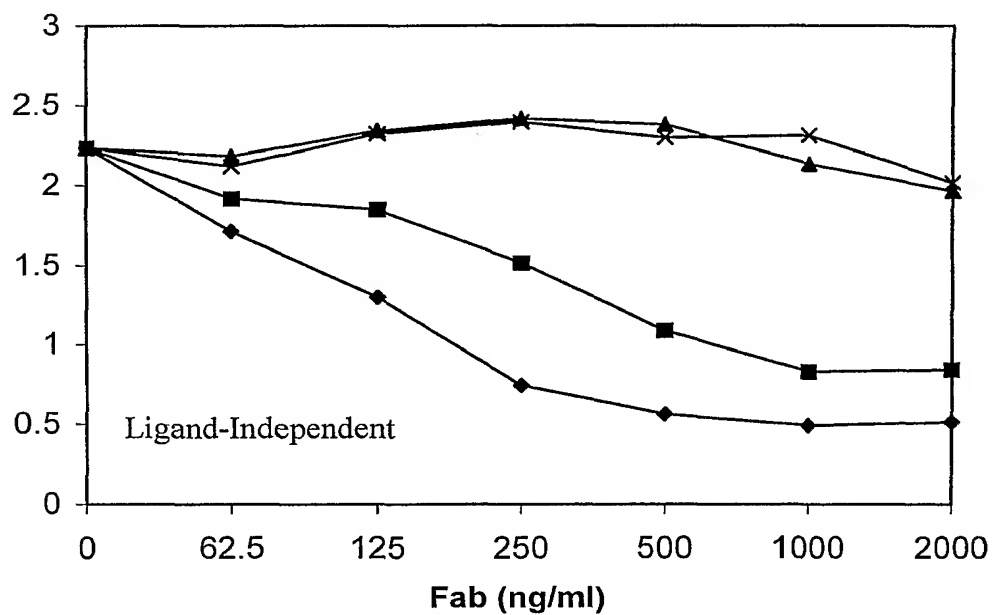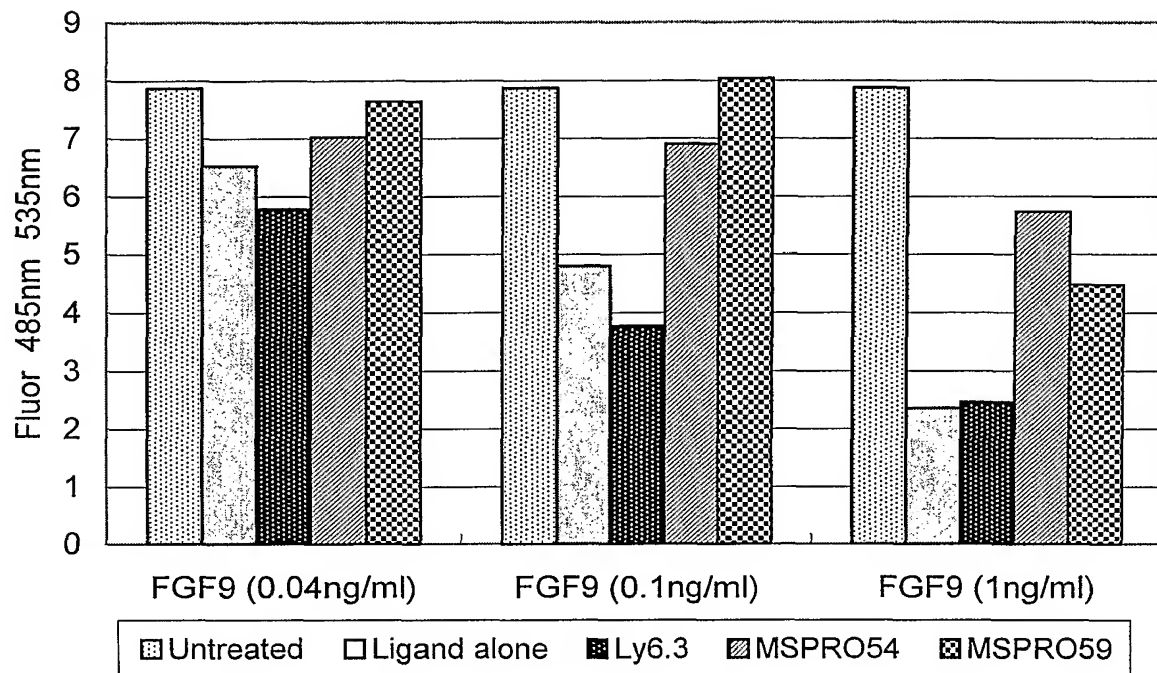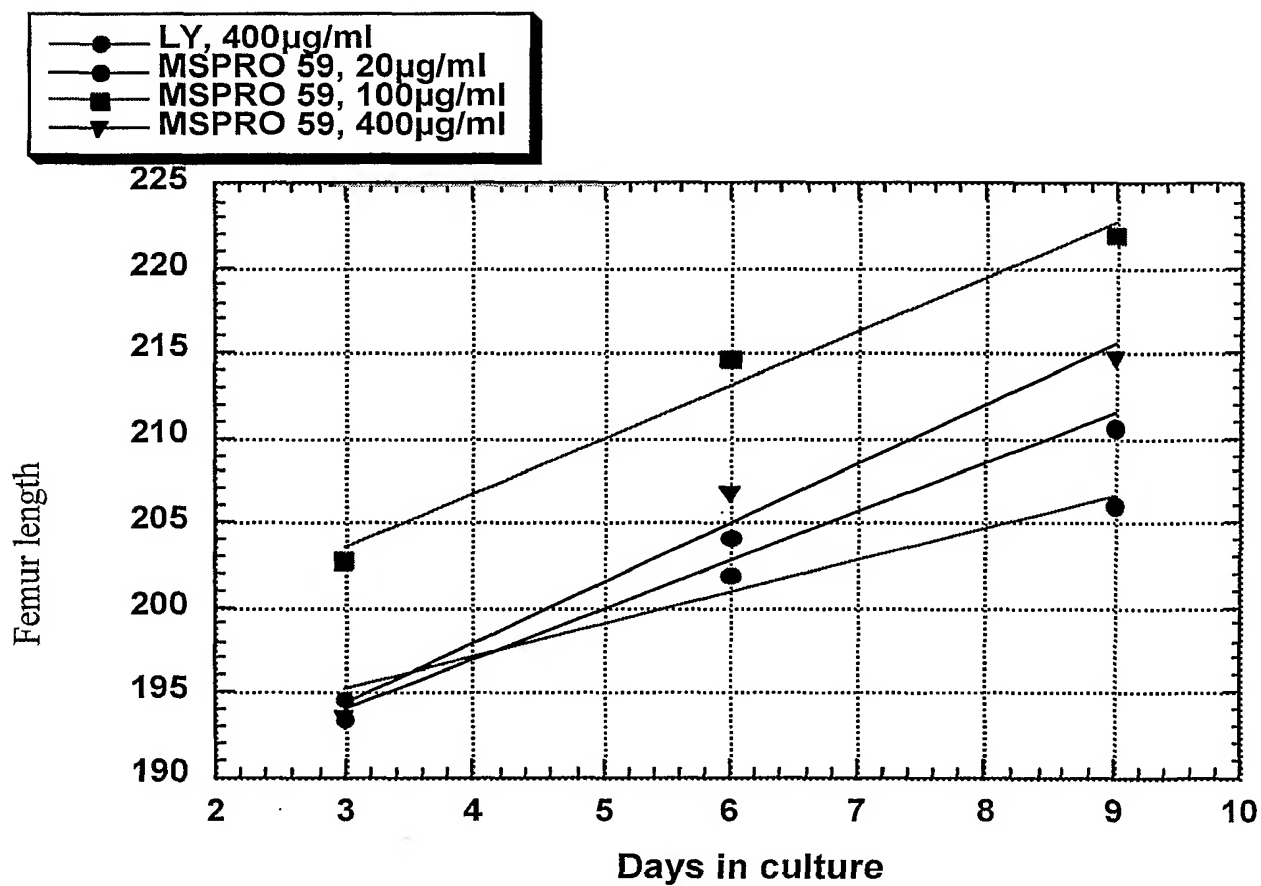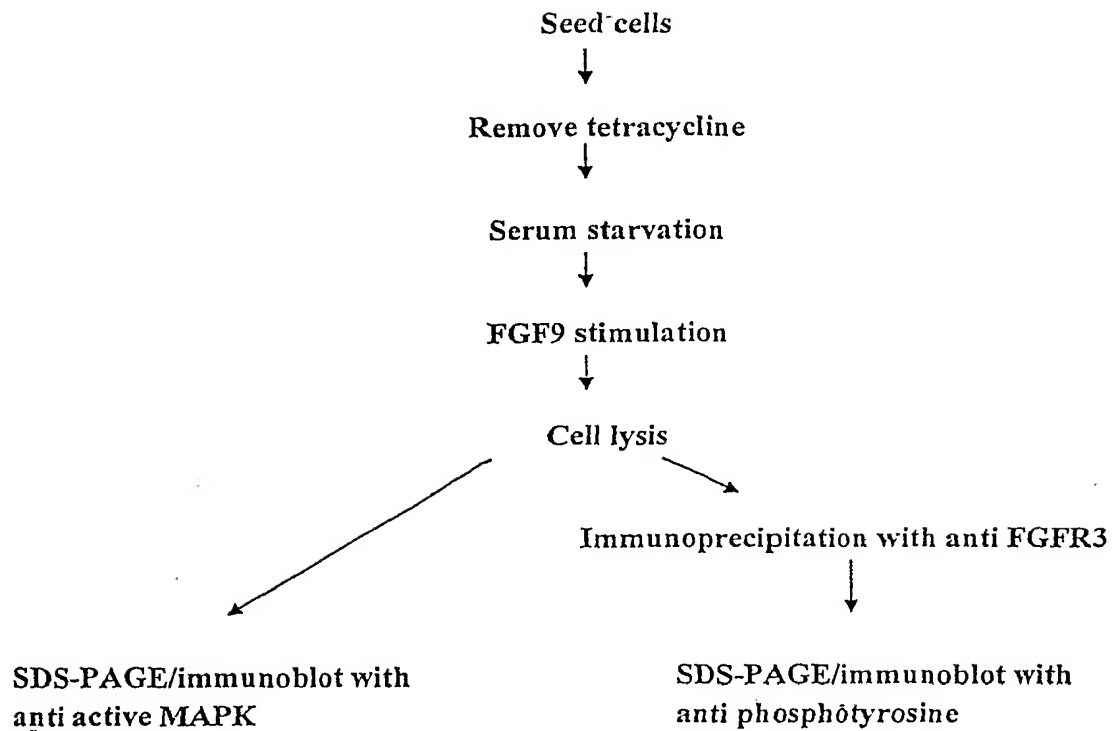
FIG.21
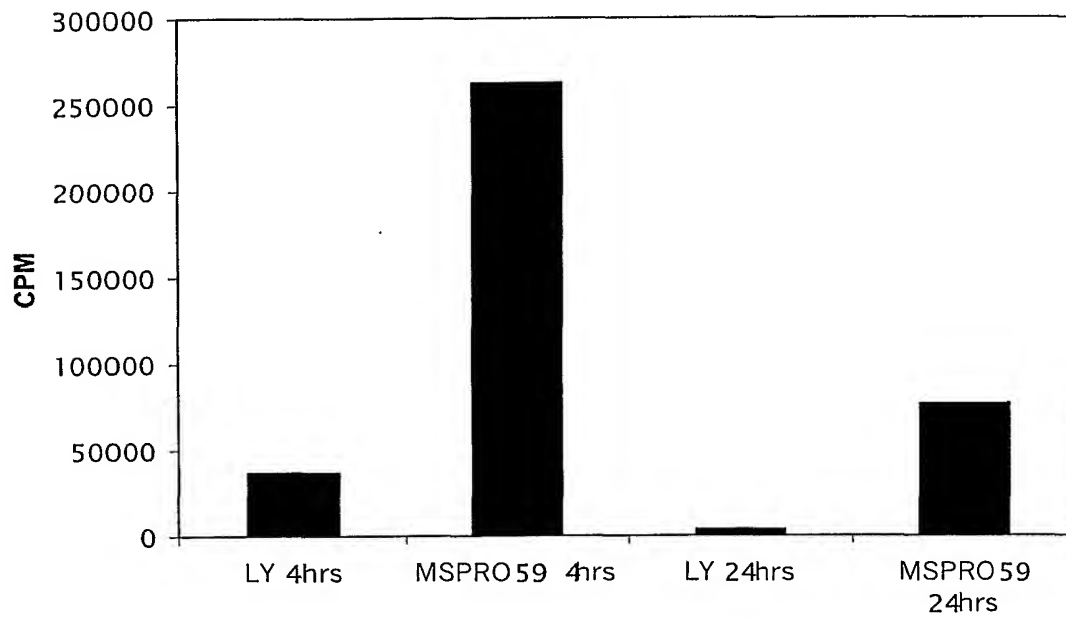
Figure 22

Figure 23
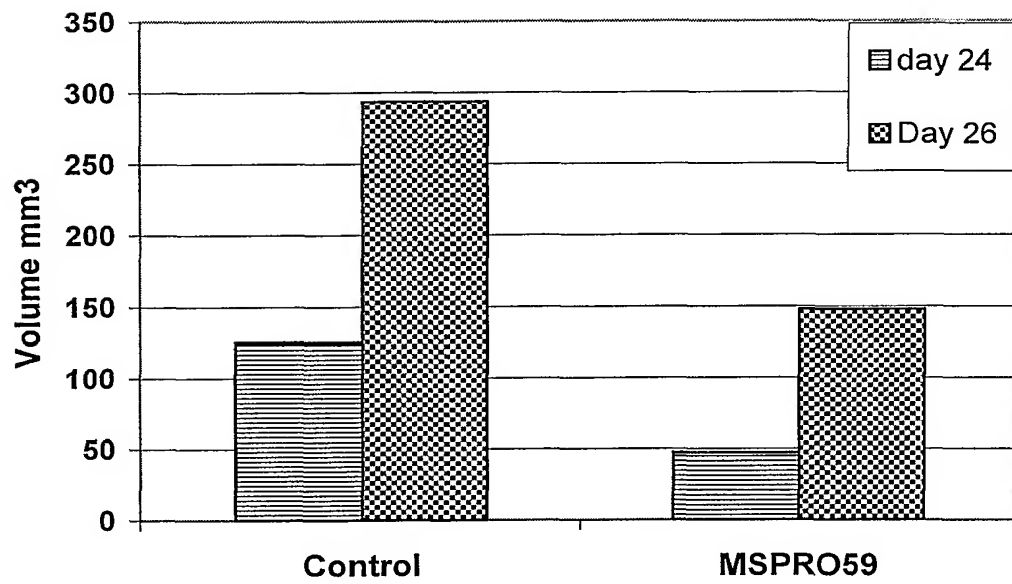
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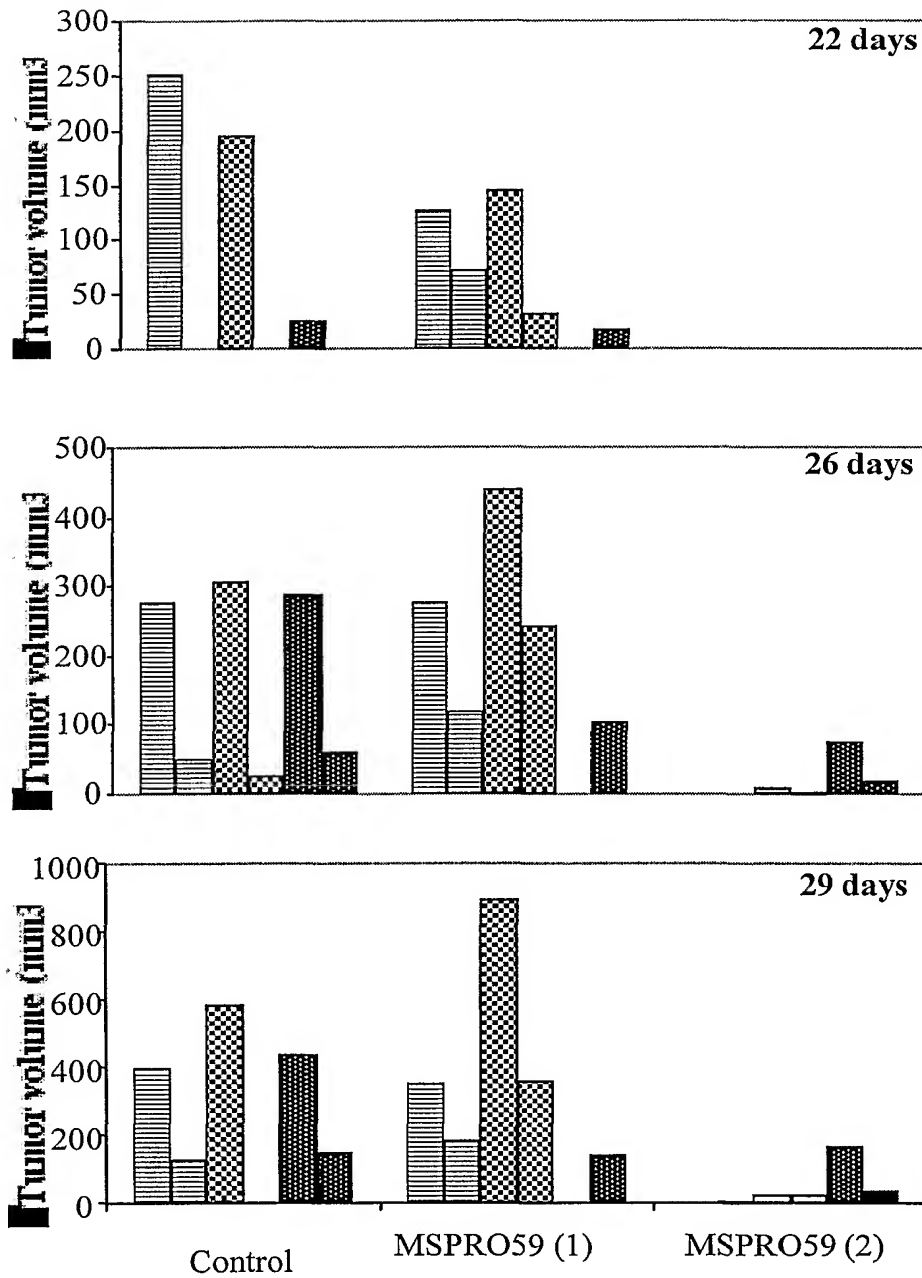
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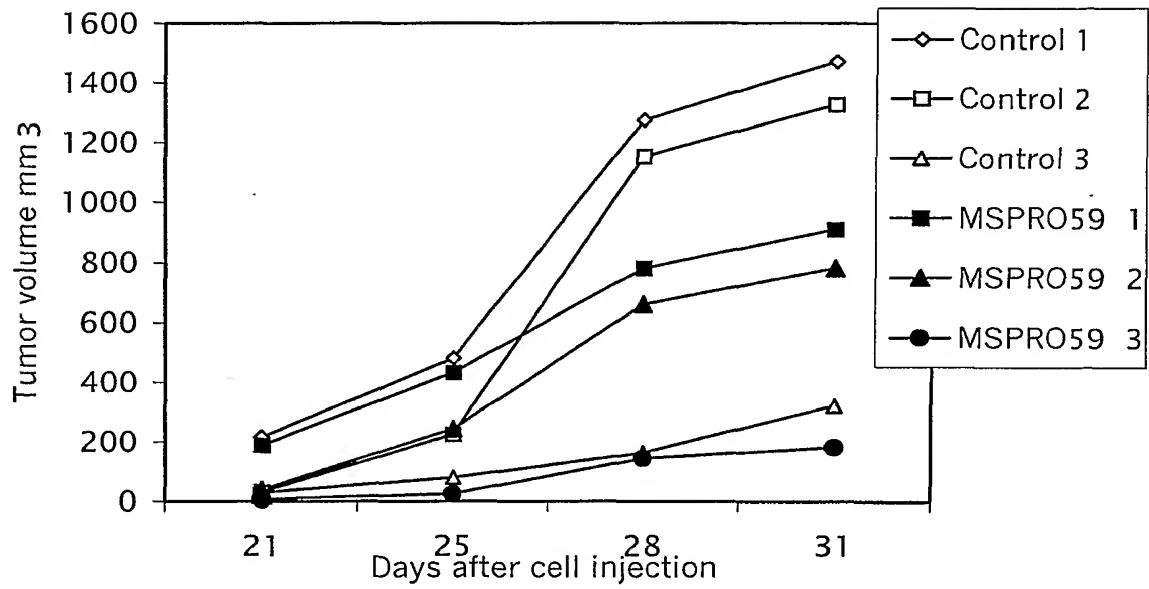
Figure 25B

25/50

Figure 26

PBS   MSPRO59 sc

26/50

Figure 27

Figure 28A

M13 Reverse primer

*Ban*H I (191)

RNAI

pMORPH®x9_Fab
5020 bp

CL
lambda

ColEI Ext2

Origin RNAII

Primer

replication start

SD
SEQ

LI (2864)

lacI

Recognition
stem loop

28/50
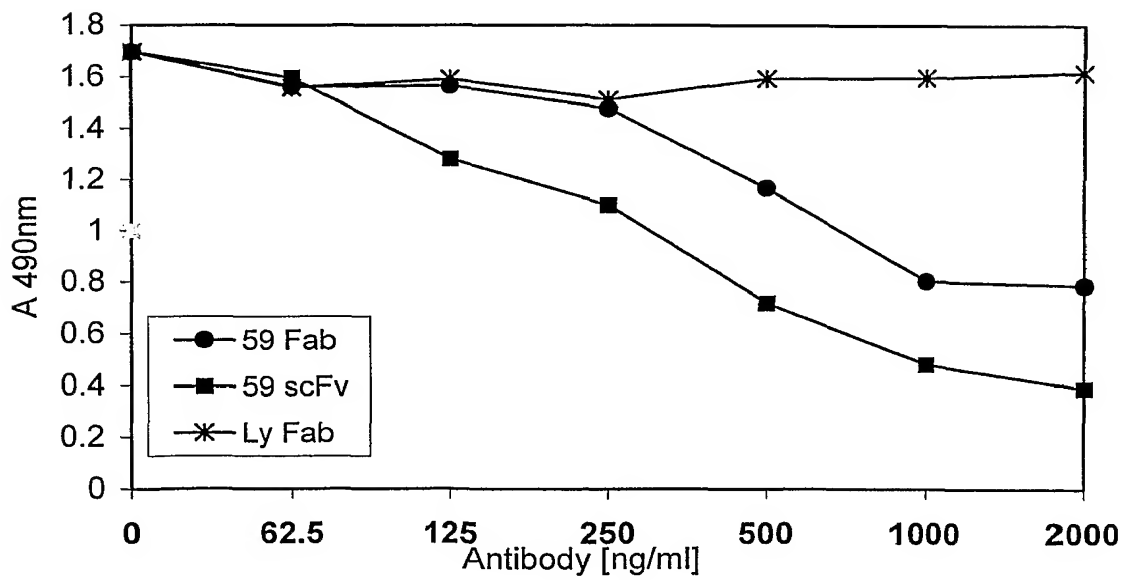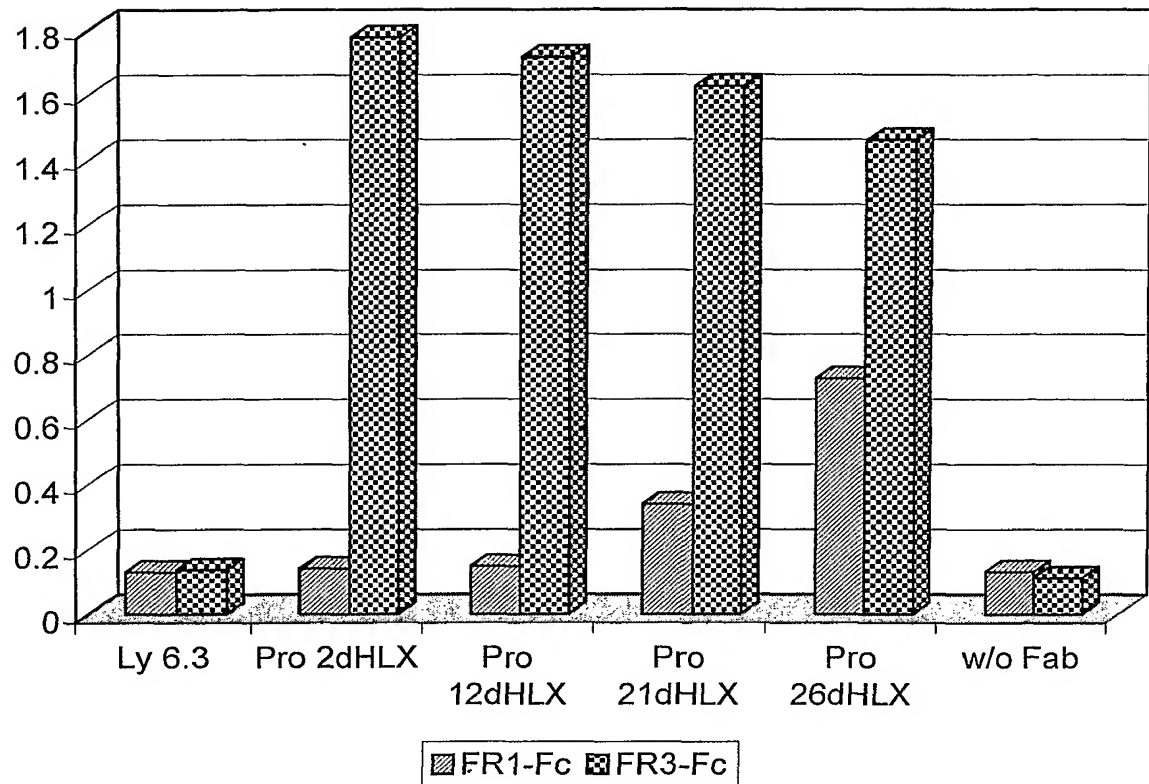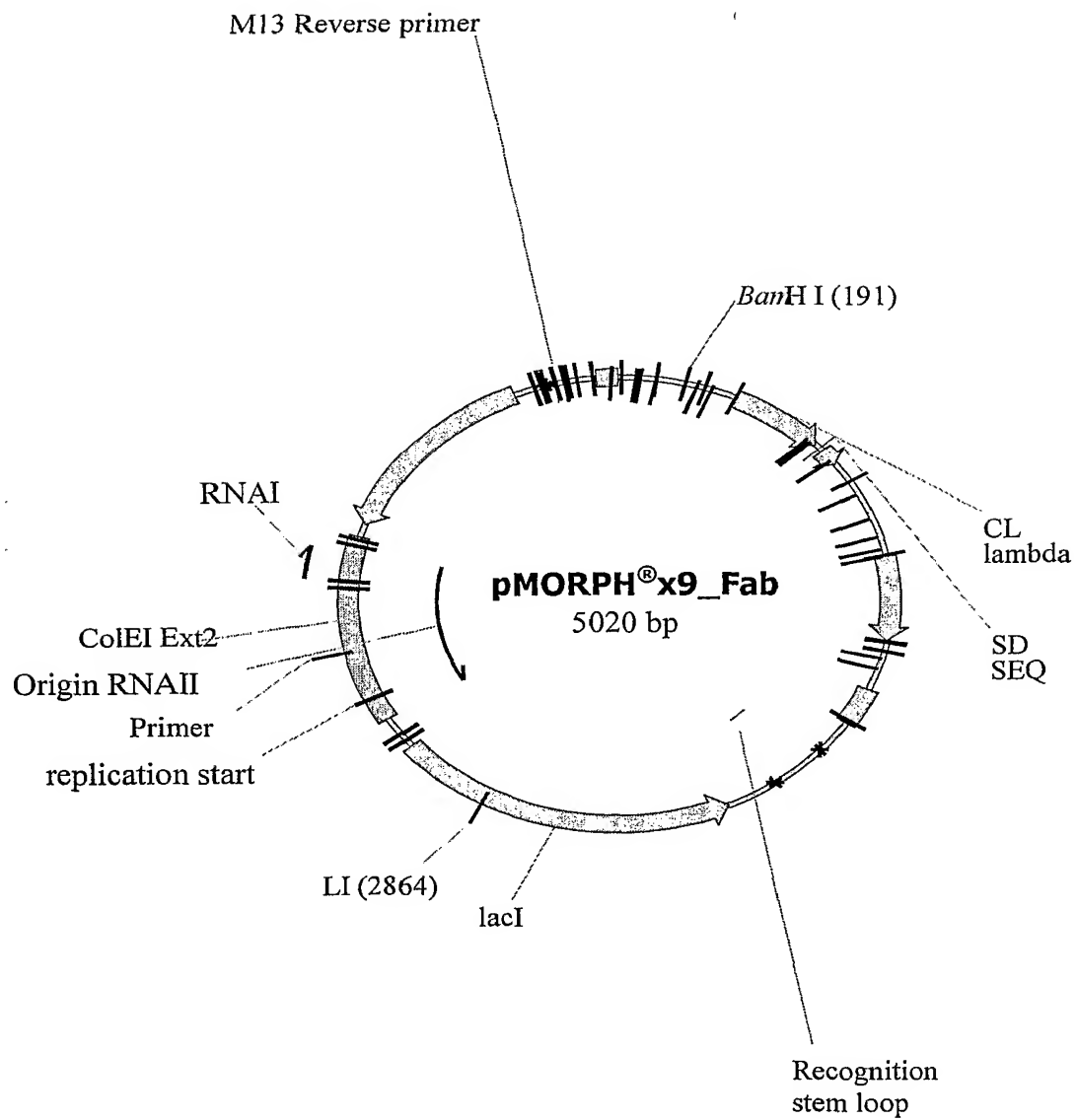
Figure 28B

EcoRV   SexAI

SEQ ID NO:52 1 ATCGTGCTGA CCCAGCCGCC TTCAGTGAGT GGCGCACCAG GTCAGCGTGT
                         TAGCACGACT GGGTCGGCGG AAGTCACTCA CCGCGTGGTC CAGTCGCACA

  51 GACCATCTCG TGTAGCGGCA GCAGCAGCAA CATTGGCAGC AACTATGTGA
       CTGGTAGAGC ACATCGCCGT CGTCGTCGTT GTAACCGTCG TTGATACACT

                                            XmaI

KpnI   SmaI

Acc65I   AvaI

 101 GCTGGTACCA GCAGTTGCCC GGGACGGCGC CGAAACTGCT GATTTATGAT
       CGACCATGGT CGTCAACGGG CCCTGCCGCG CTTTGACGA CTAAATACTA

       Bsu36I   BamHI

 151 AACAACCAGC GTCCCTCAGG CGTGCCGGAT CGTTTTAGCG GATCCAAAAG
       TTGTTGGTCG CAGGGAGTCC GCACGGCCTA GCAAAATCGC CTAGGTTTTC

                    BpuAI

                    BbsI

 201 CGGCACCAGC GCGAGCCTTG CGATTACGGG CCTGCAAAGC GAAGACGAAG
       GCCGTGGTCG CGCTCGGAAC GCTAATGCCC GGACGTTTCG CTTCTGCTTC

              Bsu36I

 251 CGGATTATTA TTGCCAGAGC TATGACATGC CTCAGGCTGT GTTTGGCGGC
       GCCTAATAAT AACGGTCTCG ATACTGTACG GAGTCCGACA CAAACCGCCG

       MscI   DraIII

 301 GGCACGAAGT TTAACCGTTC TTGGCCAGCC GAAAGCCGCA CCGAGTGTGA
       CCGTGCTTCA AATTGGCAAG AACCGGTCGG CTTTCGGCGT GGCTCACACT

 351 CGCTGTTTCC GCCGAGCAGC GAAGAATTGC AGGCGAACAA AGCGACCCTG
       GCGACAAAGG CGGCTCGTCG CTTCTTAACG TCCGCTTGTT TCGCTGGGAC

 401 GTGTGCCTGA TTAGCGACTT TTATCCGGGA GCCGTGACAG TGGCCTGGAA
       CACACGGACT AATCGCTGAA AATAGGCCCT CGGCACTGTC ACCGGACCTT

 451 GGCAGATAGC AGCCCCGTCA AGGCGGGAGT GGAGACCACC ACACCCTCCA
       CCGTCTATCG TCGGGGCAGT TCCGCCCTCA CCTCTGGTGG TGTGGGAGGT
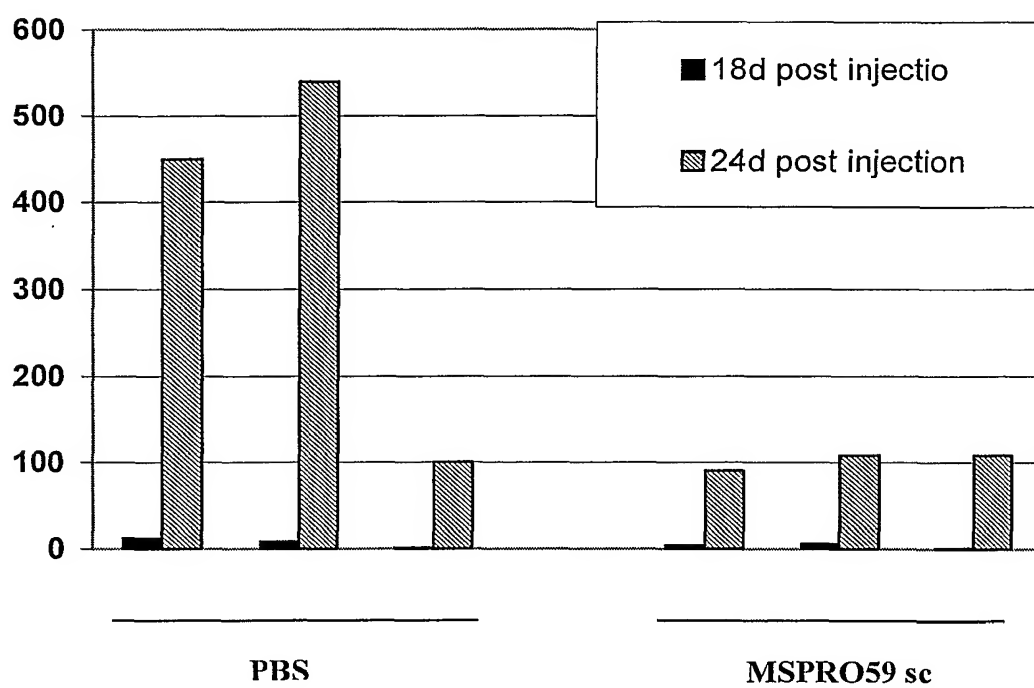
 501 AACAAAGCAA CAACAAGTAC GCGGCCAGCA GCTATCTGAG CCTGACGCCT
       TTGTTTCGTT GTTGTTCATG CGCCGGTCGT CGATAGACTC GGACTGCGGA

 551 GAGCAGTGGA AGTCCCACAG AAGCTACAGC TGCCAGGTCA CGCATGAGGG
       CTCGTCACCT TCAGGGTGTC TTCGATGTCG ACGGTCCAGT GCGTACTCCC

           StuI   SphI

601 GAGCACCGTG GAAAAAACCG TTGCGCCGAC TGAGGCCTGA TAAGCATGCG
    CTCGTGGCAC CTTTTTTGGC AACGCGGCTG ACTCCGGACT ATTCGTACGC

651 TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC ACTCTTACCG
    ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG TGAGAATGGC

                    MfeI
                    ~~~~~~

701 TTGCTCTTCA CCCCTGTTAC CAAAGCCCAG GTGCAATTGA AAGAAAGCGG
    AACGAGAAGT GGGGACAATG GTTTCGGGTC CACGTTAACT TTCTTTCGCC

                    BspEI
                     ~

751 CCCGGCCCTG GTGAAACCGA CCCAAACCCT GACCCTGACC TGTACCTTTT
    GGGCCGGGAC CACTTTGGCT GGGTTTGGGA CTGGGACTGG ACATGGAAAA

        BspEI
        ~~~~~~

801 CCGGATTTAG CCTGTCCACG TCTGGCGTTG CGTGGGCTG GATTCGCCAG
    GGCCTAAATC GGACAGGTGC AGACCGCAAC CGCACCCGAC CTAAGCGGTC

            XhoI
            ~~~~~~~
            AvaI
            ~~~~~~~

851 CCGCCTGGGA AAGCCCTCGA GTGGCTGGCT CTGATTGATT GGGATGATGA
    GGCGGACCCT TTCGGGAGCT CACCGACCGA GACTAACTAA CCCTACTACT

901 TAAGTATTAT AGCACCAGCC TGAAAACGCG TCTGACCATT AGCAAAGATA
    ATTCATAATA TCGTGGTCGG ACTTTTGCGC AGACTGGTAA TCGTTTCTAT

        BstBI
        ~~~~~~~
        SfuI
        ~~~~~~~
        NspV
        ~~~~~~~

951 CTTCGAAAAA TCAGGTGGTG CTGACTATGA CCAACATGGA CCCGGTGGAT
    GAAGCTTTTT AGTCCACCAC GACTGATACT GGTTGTACCT GGGCCACCTA

        BssHII
        ~~~~~~~

1001 ACGGCCACCT ATTATTGCGC GCGTTCTCCT CGTTATCGTG GTGCTTTTGA
     TGCCGGTGGA TAATAACGCG CGCAAGAGGA GCAATAGCAC CACGAAAACT

                BlpI
                ~~~~~~~
        StyI   CelII
        ~~~~~~~   ~~~~~~~

1051 TTATTGGGGC CAAGGCACCC TGGTGACGGT TAGCTCAGCG TCGACCAAAG
     AATAACCCCG GTTCCGTGGG ACCACTGCCA ATCGAGTCGC AGCTGGTTTC

1101 GTCCAAGCGT GTTTCCGCTG GCTCCGAGCA GCAAAAGCAC CAGCGGCGGC
     CAGGTTCGCA CAAAGGCGAC CGAGGCTCGT CGTTTTCGTG GTCGCCGCCG

1151 ACGGCTGCCC TGGGCTGCCT GGTTAAAGAT TATTTCCCGG AACCAGTCAC
     TGCCGACGGG ACCCGACGGA CCAATTTCTA ATAAAGGGCC TTGGTCAGTG

30/50

1201 CGTGAGCTGG AACAGCGGGG CGCTGACCAG CGGCGTGCAT ACCTTTCCGG
     GCACTCGACC TTGTCGCCCC GCGACTGGTC GCCGCACGTA TGGAAAGGCC

1251 CGGTGCTGCA AAGCAGCGGC CTGTATAGCC TGAGCAGCGT TGTGACCGTG
     GCCACGACGT TTCGTCGCCG GACATATCGG ACTCGTCGCA ACACTGGCAC

1301 CCGAGCAGCA GCTTAGGCAC TCAGACCTAT ATTTGCAACG TGAACCATAA
     GGCTCGTCGT CGAATCCGTG AGTCTGGATA TAAACGTTGC ACTTGGTATT

                          EcoRI
                          ~~~~~

1351 ACCGAGCAAC ACCAAAGTGG ATAAAAAGT GGAACCGAAA AGCGAATTCG
     TGGCTCGTTG TGGTTTCACC TATTTTTCA CCTTGGCTTT TCGCTTAAGC

                          BssHII
                          ~~~~~

1401 ACTATAAAGA TGACGATGAC AAAGGCGCGC CGTGGAGCCA CCCGCAGTTT
     TGATATTTCT ACTGCTACTG TTTCCGCGCG GCACCTCGGT GGGCGTCAAA

              HindIII
              ~~~~~

1451 GAAAAATGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
     CTTTTTACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
              OGIII3 100.0%
              ===================

1501 ACATTTTTTT TGTCTGCCGT TTAATTAAAG GGGGGGGGGG GCCGGCCTGG
     TGTAAAAAAA ACAGACGGCA AATTAATTTC CCCCCCCCCC CGGCCGGACC

1551 GGGGGGGTGT ACATGAAATT GTAAACGTTA ATATTTTGTT AAAATTCGCG
     CCCCCCCACA TGTACTTTAA CATTTGCAAT TATAAAACAA TTTTAAGCGC

1601 TTAAATTTTT GTTAAATCAG CTCATTTTTT AACCAATAGG CCGAAATCGG
     AATTTAAAAA CAATTTAGTC GAGTAAAAAA TTGGTTATCC GGCTTTAGCC

1651 CAAAATCCCT TATAAATCAA AAGAATAGAC CGAGATAGGG TTGAGTGTTG
     GTTTTAGGGA ATATTTAGTT TTCTTATCTG GCTCTATCCC AACTCACAAC

1701 TTCCAGTTTG GAACAAGAGT CCACTATTAA AGAACGTGGA CTCCAACGTC
     AAGGTCAAAC CTTGTTCTCA GGTGATAATT TCTTGCACCT GAGGTTGCAG

1751 AAAGGGCGAA AAACCGTCTA TCAGGGCGAT GGCCCACTAC GAGAACCATC
     TTTCCCGCTT TTTGGCAGAT AGTCCCGCTA CCGGGTGATG CTCTTGGTAG

1801 ACCCTAATCA AGTTTTTTGG GGTCGAGGTG CCGTAAAGCA CTAAATCGGA
     TGGGATTAGT TCAAAAAACC CCAGCTCCAC GGCATTTCGT GATTTAGCCT

1851 ACCCTAAAGG GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC
     TGGGATTTCC CTCGGGGGCT AAATCTCGAA CTGCCCCTTT CGGCCGCTTG

1901 GTGGCGAGAA AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT
     CACCGCTCTT TCCTTCCCTT CTTTCGCTTT CCTCGCCCGC GATCCCGCGA

1951 GGCAAGTGTA GCGGTCACGC TGCGCGTAAC CACCACACCC GCCGCGCTTA
     CCGTTCACAT CGCCAGTGCG ACGCGCATTG GTGGTGTGGG CGGCGCGAAT

31/50

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2001 ATGCGCCGCT ACAGGGCGCG TGCTAGACTA GTGTTTAAAC CGGACCGGGG
     TACGCGGCGA TGTCCCGCGC ACGATCTGAT CACAAATTTG GCCTGGCCCC

2051 GGGGGCTTAA GTGGGCTGCA AAACAAAACG GCCTCCTGTC AGGAAGCCGC
     CCCCCGAATT CACCCGACGT TTTGTTTTGC CGGAGGACAG TCCTTCGGCG

2101 TTTTATCGGG TAGCCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG
     AAAATAGCCC ATCGGAGTGA CGGGCGAAAG GTCAGCCCTT TGGACAGCAC

2151 CCAGCTGCAT CAGTGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA
     GGTCGACGTA GTCACTTAGC CGGTTGCGCG CCCCTCTCCG CCAAACGCAT

2201 TTGGGAGCCA GGGTGGTTTT TCTTTTCACC AGTGAGACGG GCAACAGCTG
     AACCCTCGGT CCCACCAAAA AGAAAAGTGG TCACTCTGCC CGTTGTCGAC

2251 ATTGCCCTTC ACCGCCTGGC CCTGAGAGAG TTGCAGCAAG CGGTCCACGC
     TAACGGGAAG TGGCGGACCG GGACTCTCTC AACGTCGTTC GCCAGGTGCG

2301 TGGTTTGCCC CAGCAGGCGA AAATCCTGTT TGATGGTGGT CAGCGGCGGG
     ACCAAACGGG GTCGTCCGCT TTTAGGACAA ACTACCACCA GTCGCCGCCC

2351 ATATAACATG AGCTGTCCTC GGTATCGTCG TATCCCACTA CCGAGATGTC
     TATATTGTAC TCGACAGGAG CCATAGCAGC ATAGGGTGAT GGCTCTACAG

2401 CGCACCAACG CGCAGCCCGG ACTCGGTAAT GGCACGCATT GCGCCCAGCG
     GCGTGGTTGC GCGTCGGGCC TGAGCCATTA CCGTGCGTAA CGCGGGTCGC

2451 CCATCTGATC GTTGGCAACC AGCATCGCAG TGGGAACGAT GCCCTCATTC
     GGTAGACTAG CAACCGTTGG TCGTAGCGTC ACCCTTGCTA CGGGAGTAAG

2501 AGCATTTGCA TGGTTTGTTG AAAACCGGAC ATGGCACTCC AGTCGCCTTC
     TCGTAAACGT ACCAAACAAC TTTTGGCCTG TACCGTGAGG TCAGCGGAAG

2551 CCGTTCCGCT ATCGGCTGAA TTTGATTGCG AGTGAGATAT TTATGCCAGC
     GGCAAGGCGA TAGCCGACTT AAACTAACGC TCACTCTATA AATACGGTCG

2601 CAGCCAGACG CAGACGCGCC GAGACAGAAC TTAATGGGCC AGCTAACAGC
     GTCGGTCTGC GTCTGCGCGG CTCTGTCTTG AATTACCCGG TCGATTGTCG

2651 GCGATTTGCT GGTGGCCCAA TGCGACCAGA TGCTCCACGC CCAGTCGCGT
     CGCTAAACGA CCACCGGGTT ACGCTGGTCT ACGAGGTGCG GGTCAGCGCA

2701 ACCGTCCTCA TGGGAGAAAA TAATACTGTT GATGGGTGTC TGGTCAGAGA
     TGGCAGGAGT ACCCTCTTTT ATTATGACAA CTACCCACAG ACCAGTCTCT

2751 CATCAAGAAA TAACGCCGGA ACATTAGTGC AGGCAGCTTC CACAGCAATA
     GTAGTTCTTT ATTGCGGCCT TGTAATCACG TCCGTCGAAG GTGTCGTTAT

2801 GCATCCTGGT CATCCAGCGG ATAGTTAATA ATCAGCCCAC TGACACGTTG
     CGTAGGACCA GTAGGTCGCC TATCAATTAT TAGTCGGGTG ACTGTGCAAC
```

ApaLI
~~~~~~

```
2851 CGCGAGAAGA TTGTGCACCG CCGCTTTACA GGCTTCGACG CCGCTTCGTT
     GCGCTCTTCT AACACGTGGC GGCGAAATGT CCGAAGCTGC GGCGAAGCAA

2901 CTACCATCGA CACGACCACG CTGGCACCCA GTTGATCGGC GCGAGATTTA
```

32/50

GATGGTAGCT GTGCTGGTGC GACCGTGGGT CAACTAGCCG CGCTCTAAAT

2951 ATCGCCGCGA CAATTTGCGA CGGCGCGTGC AGGGCCAGAC TGGAGGTGGC
     TAGCGGCGCT GTTAAACGCT GCCGCGCACG TCCCGGTCTG ACCTCCACCG

3001 AACGCCAATC AGCAACGACT GTTTGCCCGC CAGTTGTTGT GCCACGCGGT
     TTGCGGTTAG TCGTTGCTGA CAAACGGGCG GTCAACAACA CGGTGCGCCA

3051 TAGGAATGTA ATTCAGCTCC GCCATCGCCG CTTCCACTTT TTCCCGCGTT
     ATCCTTACAT TAAGTCGAGG CGGTAGCGGC GAAGGTGAAA AAGGGCGCAA

3101 TTCGCAGAAA CGTGGCTGGC CTGGTTCACC ACGCGGGAAA CGGTCTGATA
     AAGCGTCTTT GCACCGACCG GACCAAGTGG TGCGCCCTTT GCCAGACTAT

3151 AGAGACACCG GCATACTCTG CGACATCGTA TAACGTTACT GGTTTCACAT
     TCTCTGTGGC CGTATGAGAC GCTGTAGCAT ATTGCAATGA CCAAAGTGTA

3201 TCACCACCCT GAATTGACTC TCTTCCGGGC GCTATCATGC CATACCGCGA
     AGTGGTGGGA CTTAACTGAG AGAAGGCCCG CGATAGTACG GTATGGCGCT

3251 AAGGTTTTGC GCCATTCGAT GCTAGCCATG TGAGCAAAAG GCCAGCAAAA
     TTCCAAAACG CGGTAAGCTA CGATCGGTAC ACTCGTTTTC CGGTCGTTTT

3301 GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC
     CCGGTCCTTG GCATTTTTCC GGCGCAACGA CCGCAAAAAG GTATCCGAGG

3351 GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA
     CGGGGGGACT GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT CTCCACCGCT

3401 AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT
     TTGGGCTGTC CTGATATTTC TATGGTCCGC AAAGGGGGAC CTTCGAGGGA

3451 CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT
     GCACGCGAGA GGACAAGGCT GGGACGGCGA ATGGCCTATG GACAGGCGGA

3501 TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC ATAGCTCACG CTGTAGGTAT
     AAGAGGGAAG CCCTTCGCAC CGCGAAAGAG TATCGAGTGC GACATCCATA

                         ApaLI
                         ~~~~~~
3551 CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
     GAGTCAAGCC ACATCCAGCA AGCGAGGTTC GACCCGACAC ACGTGCTTGG

3601 CCCCGTTCAG CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT
     GGGGCAAGTC GGGCTGGCGA CGCGGAATAG GCCATTGATA GCAGAACTCA

3651 CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC
     GGTTGGGCCA TTCTGTGCTG AATAGCGGTG ACCGTCGTCG GTGACCATTG

3701 AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG
     TCCTAATCGT CTCGCTCCAT ACATCCGCCA CGATGTCTCA AGAACTTCAC

3751 GTGGCCTAAC TACGGCTACA CTAGAAGAAC AGTATTTGGT ATCTGCGCTC
     CACCGGATTG ATGCCGATGT GATCTTCTTG TCATAAACCA TAGACGCGAG

3801 TGCTGTAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC
     ACGACATCGG TCAATGGAAG CCTTTTTCTC AACCATCGAG AACTAGGCCG

33/50

3851 AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT
     TTTGTTTGGT GGCGACCATC GCCACCAAAA AAACAAACGT TCGTCGTCTA

5

3901 TACGCGCAGA AAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG
     ATGCGCGTCT TTTTTTCCTA GAGTTCTTCT AGGAAACTAG AAAAGATGCC

3951 GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCAGA
     CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA AAACCAGTCT

10

4001 TCTAGCACCA GGCGTTTAAG GGCACCAATA ACTGCCTTAA AAAAATTACG
     AGATCGTGGT CCGCAAATTC CCGTGGTTAT TGACGGAATT TTTTTAATGC

4051 CCCCGCCCTG CCACTCATCG CAGTACTGTT GTAATTCATT AAGCATTCTG
     GGGGCGGGAC GGTGAGTAGC GTCATGACAA CATTAAGTAA TTCGTAAGAC

15

4101 CCGACATGGA AGCCATCACA AACGGCATGA TGAACCTGAA TCGCCAGCGG
     GGCTGTACCT TCGGTAGTGT TTGCCGTACT ACTTGGACTT AGCGGTCGCC

20 4151 CATCAGCACC TTGTCGCCTT GCGTATAATA TTTGCCCATA GTGAAAACGG
     GTAGTCGTGG AACAGCGGAA CGCATATTAT AAACGGGTAT CACTTTTGCC

4201 GGGCGAAGAA GTTGTCCATA TTGGCTACGT TTAAATCAAA ACTGGTGAAA
     CCCGCTTCTT CAACAGGTAT AACCGATGCA AATTTAGTTT TGACCACTTT

25

4251 CTCACCCAGG GATTGGCTGA GACGAAAAAC ATATTCTCAA TAAACCCTTT
     GAGTGGGTCC CTAACCGACT CTGCTTTTTG TATAAGAGTT ATTTGGGAAA

4301 AGGGAAATAG GCCAGGTTTT CACCGTAACA CGCCACATCT TGCGAATATA
     TCCCTTTATC CGGTCCAAAA GTGGCATTGT GCGGTGTAGA ACGCTTATAT

30

4351 TGTGTAGAAA CTGCCGGAAA TCGTCGTGGT ATTCACTCCA GAGCGATGAA
     ACACATCTTT GACGGCCTTT AGCAGCACCA TAAGTGAGGT CTCGCTACTT

35 4401 AACGTTTCAG TTTGCTCATG GAAAACGGTG TAACAAGGGT GAACACTATC
     TTGCAAAGTC AAACGAGTAC CTTTTGCCAC ATTGTTCCCA CTTGTGATAG

4451 CCATATCACC AGCTCACCGT CTTTCATTGC CATACGGAAC TCCGGGTGAG
     GGTATAGTGG TCGAGTGGCA GAAAGTAACG GTATGCCTTG AGGCCCACTC

40

4501 CATTCATCAG GCGGGCAAGA ATGTGAATAA AGGCCGGATA AAACTTGTGC
     GTAAGTAGTC CGCCCGTTCT TACACTTATT TCCGGCCTAT TTTGAACACG

4551 TTATTTTTCT TTACGGTCTT TAAAAAGGCC GTAATATCCA GCTGAACGGT
     AATAAAAAGA AATGCCAGAA ATTTTCCGG CATTATAGGT CGACTTGCCA

45

4601 CTGGTTATAG GTACATTGAG CAACTGACTG AAATGCCTCA AAATGTTCTT
     GACCAATATC CATGTAACTC GTTGACTGAC TTTACGGAGT TTTACAAGAA

50 4651 TACGATGCCA TTGGGATATA TCAACGGTGG TATATCCAGT GATTTTTTTC
     ATGCTACGGT AACCCTATAT AGTTGCCACC ATATAGGTCA CTAAAAAAAG

4701 TCCATTTTAG CTTCCTTAGC TCCTGAAAAT CTCGATAACT CAAAAAATAC
     AGGTAAAATC GAAGGAATCG AGGACTTTTA GAGCTATTGA GTTTTTTATG

55

4751 GCCCGGTAGT GATCTTATTT CATTATGGTG AAAGTTGGAA CCTCACCCGA
     CGGGCCATCA CTAGAATAAA GTAATACCAC TTTCAACCTT GGAGTGGGCT

34/50

SUBSTITUTE SHEET (RULE 26)

4801 CGTCTAATGT GAGTTAGCTC ACTCATTAGG CACCCCAGGC TTTACACTTT
      GCAGATTACA CTCAATCGAG TGAGTAATCC GTGGGGTCCG AAATGTGAAA

4851 ATGCTTCCGG CTCGTATGTT GTGTGGAATT GTGAGCGGAT AACAATTTCA
      TACGAAGGCC GAGCATACAA CACACCTTAA CACTCGCCTA TTGTTAAAGT

      M13 Reverse primer 100.0%   XbaI
      ===============   ~~~~~~

4901 CACAGGAAAC AGCTATGACC ATGATTACGA ATTTCTAGAT AACGAGGGCA
      GTGTCCTTTG TCGATACTGG TACTAATGCT TAAAGATCTA TTGCTCCCGT

4951 AAAAATGAAA AAGACAGCTA TCGCGATTGC AGTGGCACTG GCTGGTTTCG
      TTTTTACTTT TTCTGTCGAT AGCGCTAACG TCACCGTGAC CGACCAAAGC

            EcoRV
            ~~~

5001 CTACCGTAGC GCAGGCCGAT
      GATGGCATCG CGTCCGGCTA

35/50

Figure 29A

lacZ´(21bp)

SD

lac mRNA

start

lac operator region

SD

omp A

CRP site

region

Vk3

cat promoter

CM(R)(657bp)

CL kappa(315 bp)

cat terminator

pho A

mutation

mutation

pMorph18 Fab VH3k3 example II

4151 bp

VH3

mutation

mutation

ORi

f1 origin

>A

CH1(306 bp)

CTgIII(471 bp)

Stop

lpp terminator

36/50

Figure 29B

lacZ'   SD   ompA
~~   ~~~~~   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
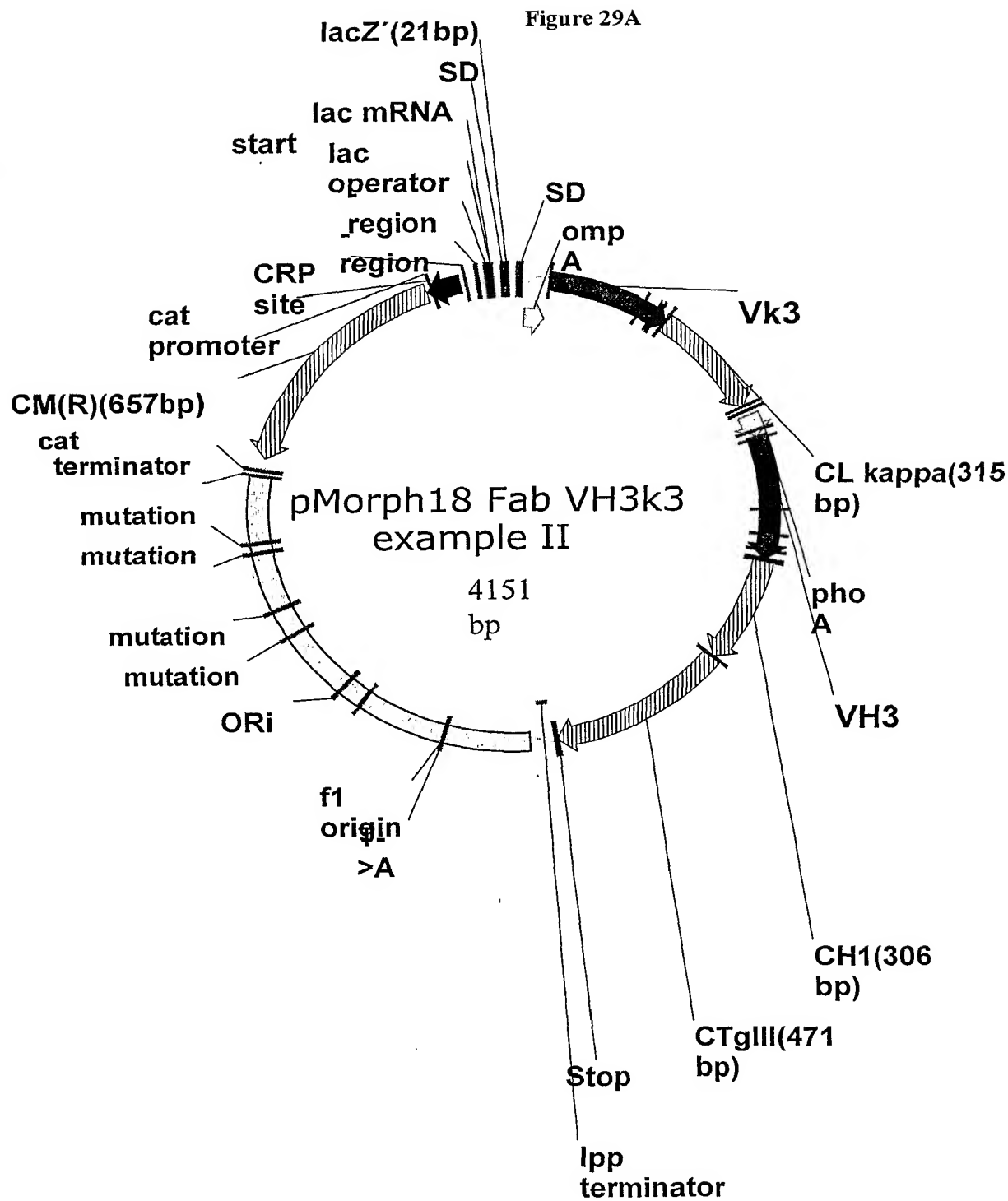
XbaI
~~~~~

5

                       M K K T A I A I A V ·

SEQ ID NO:53 TCTAGATAAC GAGGGCAAAA AATGAAAAAG ACAGCTATCG CGATTGCAGT
               AGATCTATTG CTCCCGTTTT TTACTTTTTC TGTCGATAGC GCTAACGTCA

                       Vk3
                       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

10

ompA
~~~~~~

EcoRV
~~~~~~~

15

A L A   G F A T V A Q   A D I V L T Q ·
GGCACTGGCT GGTTTCGCTA CCGTAGCGCA GGCCGATATC GTGCTGACCC
CCGTGACCGA CCAAAGCGAT GGCATCGCGT CCGGCTATAG CACGACTGGG
              Vk3
~~~~~~

20

  · S P A T L S L S P G E R A T L S
    101 AGAGCCCGGC GACCCTGAGC CTGTCTCCGG GCGAACGTGC GACCCTGAGC
           TCTCGGGCCG CTGGGACTCG GACAGAGGCC CGCTTGCACG CTGGGACTCG
               Vk3
~~~~~~

25

  C R A S Q S V S S S Y L A W Y Q Q ·
    151 TGCAGAGCGA GCCAGAGCGT GAGCAGCAGC TATCTGGCGT GGTACCAGCA
           ACGTCTCGCT CGGTCTCGCA CTCGTCGTCG ATAGACCGCA CCATGGTCGT
               Vk3
~~~~~~

30

  · K P G   Q A P R L L I Y G A S S R A ·
    201 GAAACCAGGT CAAGCACCGC GTCTATTAAT TTATGGCGCG AGCAGCCGTG
           CTTTGGTCCA GTTCGTGGCG CAGATAATTA AATACCGCGC TCGTCGGCAC
               Vk3
~~~~~~

35

  · T G V   P A R F S G S   G S G T D F
    251 CAACTGGGGT CCCGGCGCGT TTTAGCGGCT CTGGATCCGG CACGGATTTT
           GTTGACCCCA GGGCCGCGCA AAATCGCCGA GACCTAGGCC GTGCCTAAAA
               Vk3
~~~~~~

40

               BbsI
               ~~~~~~~

  T L T I S S L E P E D F A V Y Y C ·
    301 ACCCTGACCA TTAGCAGCCT GGAACCTGAA GACTTTGCGG TGTATTATTG
           TGGGACTGGT AATCGTCGGA CCTTGGACTT CTGAAACGCC ACATAATAAC

45

               Vk3
~~~~~~

               MscI
               ~~~~~~~

  · Q Q H   Y T T P   P T F G Q G T K V E ·
    351 CCAGCAGCAT TATACCACCC CGCCGACCTT GGCCAGGGT ACGAAAGTTG

50

           GGTCGTCGTA ATATGGTGGG GCGGCTGGAA ACCGGTCCCA TGCTTTCAAC
             CL kappa
~~~~~~

          Vk3

55

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

         BsiWI
         ~~~~~~~~

  · I K R   T V A A P S V F I F P P S
    401 AAATTAAACG TACGGTGGCT GCTCCGAGCG TGTTTATTTT TCCGCCGAGC

60

           TTTAATTTGC ATGCCACCGA CGAGGCTCGC ACAAATAAAA AGGCGGCTCG

37/50

CL kappa

```
        D E Q L K S G T A S V V C L L N N·
  451   GATGAACAAC TGAAAAGCGG CACGGCGAGC GTGGTGTGCC TGCTGAACAA
        CTACTTGTTG ACTTTTCGCC GTGCCGCTCG CACCACACGG ACGACTTGTT
                   CL kappa
```

```
        ·F Y P R E A K V Q W K V D N A L Q·
  501   CTTTTATCCG CGTGAAGCGA AAGTTCAGTG GAAAGTAGAC AACGCGCTGC
        GAAAATAGGC GCACTTCGCT TTCAAGTCAC CTTTCATCTG TTGCGCGACG
                   CL kappa
```

```
        ·S G N S Q E S V T E Q D S K D S
  551   AAAGCGGCAA CAGCCAGGAA AGCGTGACCG AACAGGATAG CAAAGATAGC
        TTTCGCCGTT GTCGGTCCTT TCGCACTGGC TTGTCCTATC GTTTCTATCG
                   CL kappa
```

```
        T Y S L S S T L T L S K A D Y E K·
  601   ACCTATTCTC TGAGCAGCAC CCTGACCCTG AGCAAAGCGG ATTATGAAAA
        TGGATAAGAG ACTCGTCGTG GGACTGGGAC TCGTTTCGCC TAATACTTTT
                   CL kappa
```

```
        ·H K V Y A C E V T H Q G L S S P V·
  651   ACATAAAGTG TATGCGTGCG AAGTGACCCA TCAAGGTCTG AGCAGCCCGG
        TGTATTTCAC ATACGCACGC TTCACTGGGT AGTTCCAGAC TCGTCGGGCC
              CL kappa
```

```
                   StuI      SphI
        ·T K S F N R G E A
  701   TGACTAAATC TTTTAATCGT GGCGAGGCCT GATAAGCATG CGTAGGAGAA
        ACTGATTTAG AAAATTAGCA CCGCTCCGGA CTATTCGTAC GCATCCTCTT
                   phoA
```

```
                            SapI
        M K Q S T I A L A L L P L L F·
  751   AATAAAATGA AACAAAGCAC TATTGCACTG GCACTCTTAC CGTTGCTCTT
        TTATTTTACT TTGTTTCGTG ATAACGTGAC CGTGAGAATG GCAACGAGAA
                   VH3
```

```
        phoA

        SapI         MfeI
        ~            ~
        ·T P V T K A Q V Q L V E S G G G L·
  801   CACCCCTGTT ACCAAAGCCG AAGTGCAATT GGTGGAAAGC GGCGGCGGCC
        GTGGGGACAA TGGTTTCGGC TTCACGTTAA CCACCTTTCG CCGCCGCCGG
                   VH3
```

```
        ·V Q P G G S L R L S C A A S G F
  851   TGGTGCAACC GGGCGGCAGC CTGCGTCTGA CTGCGCGGC CTCCGGATTT
        ACCACGTTGG CCCGCCGTCG GACGCAGACT CGACGCGCCG GAGGCCTAAA
                   VH3
```

```
        T F S S Y A M S W V R Q A P G K G·
  901   ACCTTTAGCA GCTATGCGAT GAGCTGGGTG CGCCAAGCCC CTGGGAAGGG
        TGGAAATCGT CGATACGCTA CTCGACCCAC GCGGTTCGGG GACCCTTCCC
                   VH3
```

38/50

·L E W V S A I S G S G G S T Y Y A·
951 TCTCGAGTGG GTGAGCGCGA TTAGCGGTAG CGGCGGCAGC ACCTATTATG
     AGAGCTCACC CACTCGCGCT AATCGCCATC GCCGCCGTCG TGGATAATAC
     VH3
     ～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～
          PmlI
          ～～～～

·D S V K G R F T I S R D N S K N
1001 CGGATAGCGT GAAAGGCCGT TTTACCATTT CACGTGATAA TTCGAAAAAC
      GCCTATCGCA CTTTCCGGCA AAATGGTAAA GTGCACTATT AAGCTTTTTG
      VH3
      ～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～

T L Y L Q M N S L R A E D T A V Y·
1051 ACCCTGTATC TGCAAATGAA CAGCCTGCGT GCGGAAGATA CGGCCGTGTA
      TGGGACATAG ACGTTTACTT GTCGGACGCA CGCCTTCTAT GCCGGCACAT
      VH3
      ～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～

       BssHII
       ～～～～～～

·Y C A R W G G D G F Y A M D Y W G·
1101 TTATTGCGCG CGTTGGGGCG GCGATGGCTT TTATGCGATG GATTATTGGG
      AATAACGCGC GCAACCCCGC CGCTACCGAA AATACGCTAC CTAATAACCC
                         CH1
                         ～～～～～～～～～～～～～～～～～～
       VH3
       ～～～～～～～～～～～～～～～～～～～～～～～～～～

          SalI
          ～～～～～～

   StyI   BlpI
   ～～～～   ～～～～～～
·Q G T L V T V S S A S T K G P S
1151 GCCAAGGCAC CCTGGTGACG GTTAGCTCAG CGTCGACCAA AGGTCCAAGC
      CGGTTCCGTG GGACCACTGC CAATCGAGTC GCAGCTGGTT TCCAGGTTCG
      CH1
      ～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～

V F P L A P S S K S T S G G T A A·
1201 GTGTTTCCGC TGGCTCCGAG CAGCAAAAGC ACCAGCGGCG GCACGGCTGC
      CACAAAGGCG ACCGAGGCTC GTCGTTTTCG TGGTCGCCGC CGTGCCGACG
      CH1
      ～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～

·L G C L V K D Y F P E P V T V S W·
1251 CCTGGGCTGC CTGGTTAAAG ATTATTTCCC GGAACCAGTC ACCGTGAGCT
      GGACCCGACG GACCAATTTC TAATAAAGGG CCTTGGTCAG TGGCACTCGA
      CH1
      ～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～

·N S G A L T S G V H T F P A V L
1301 GGAACAGCGG GGCGCTGACC AGCGGCGTGC ATACCTTTCC GGCGGTGCTG
      CCTTGTCGCC CCGCGACTGG TCGCCGCACG TATGGAAAGG CCGCCACGAC
      CH1
      ～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～

Q S S G L Y S L S S V V T V P S S·
1351 CAAAGCAGCG GCCTGTATAG CCTGAGCAGC GTTGTGACCG TGCCGAGCAG
      GTTTCGTCGC CGGACATATC GGACTCGTCG CAACACTGGC ACGGCTCGTC
      CH1
      ～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～～

·S L G T Q T Y I C N V N H K P S N·
1401 CAGCTTAGGC ACTCAGACCT ATATTTGCAA CGTGAACCAT AAACCGAGCA
      GTCGAATCCG TGAGTCTGGA TATAAACGTT GCACTTGGTA TTTGGCTCGT
      CH1   CTgIII
      ～～～～～～～～～～～～～～～～～～～～   ～～ ～～～～～～～～

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EcoRI

· T K V D K K V E P K S E F G G G
1451 ACACCAAAGT GGATAAAAAA GTGGAACCGA AAAGCGAATT CGGGGGAGGG
     TGTGGTTTCA CCTATTTTTT CACCTTGGCT TTTCGCTTAA GCCCCCTCCC
     CTgIII

S G S G D F D Y E K M A N A N K G ·
1501 AGCGGGAGCG GTGATTTTGA TTATGAAAAG ATGGCAAACG CTAATAAGGG
     TCGCCCTCGC CACTAAAACT AATACTTTTC TACCGTTTGC GATTATTCCC
     CTgIII

· A M T E N A D E N A L Q S D A K G ·
1551 GGCTATGACC GAAAATGCCG ATGAAAACGC GCTACAGTCT GACGCTAAAG
     CCGATACTGG CTTTTACGGC TACTTTTGCG CGATGTCAGA CTGCGATTTC
     CTgIII

· K L D S V A T D Y G A A I D G F
1601 GCAAACTTGA TTCTGTCGCT ACTGATTACG GTGCTGCTAT CGATGGTTTC
     CGTTTGAACT AAGACAGCGA TGACTAATGC CACGACGATA GCTACCAAAG
     CTgIII

I G D V S G L A N G N G A T G D F ·
1651 ATTGGTGACG TTTCCGGCCT TGCTAATGGT AATGGTGCTA CTGGTGATTT
     TAACCACTGC AAAGGCCGGA ACGATTACCA TTACCACGAT GACCACTAAA
     CTgIII

· A G S N S Q M A Q V G D G D N S P ·
1701 TGCTGGCTCT AATTCCCAAA TGGCTCAAGT CGGTGACGGT GATAATTCAC
     ACGACCGAGA TTAAGGGTTT ACCGAGTTCA GCCACTGCCA CTATTAAGTG
     CTgIII

· L M N N F R Q Y L P S L P Q S V
1751 CTTTAATGAA TAATTTCCGT CAATATTTAC CTTCCCTCCC TCAATCGGTT
     GAAATTACTT ATTAAAGGCA GTTATAAATG AAGGGAGGG AGTTAGCCAA
     CTgIII

E C R P F V F G A G K P Y E F S I ·
1801 GAATGTCGCC CTTTTGTCTT TGGCGCTGGT AAACCATATG AATTTTCTAT
     CTTACAGCGG GAAAACAGAA ACCGCGACCA TTTGGTATAC TTAAAAGATA
     CTgIII

· D C D K I N L F R G V F A F L L Y ·
1851 TGATTGTGAC AAAATAAACT TATTCCGTGG TGTCTTTGCG TTTCTTTTAT
     ACTAACACTG TTTTATTTGA ATAAGGCACC ACAGAAACGC AAAGAAAATA
     CTgIII

· V A T F M Y V F S T F A N I L R
1901 ATGTTGCCAC CTTTATGTAT GTATTTTCTA CGTTTGCTAA CATACTGCGT
     TACAACGGTG GAAATACATA CATAAAAGAT GCAAACGATT GTATGACGCA
     CTgIII

Stop   lpp terminator

HindIII

N K E S
1951 AATAAGGAGT CTTGATAAGC TTGACCTGTG AAGTGAAAAA TGGCGCAGAT
     TTATTCCTCA GAACTATTCG AACTGGACAC TTCACTTTTT ACCGCGTCTA
     lpp terminator

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2001   TGTGCGACAT TTTTTTTGTC TGCCGTTTAA TGAAATTGTA AACGTTAATA
           ACACGCTGTA AAAAAACAG ACGGCAAATT ACTTTAACAT TTGCAATTAT

f1 origin
2051   TTTTGTTAAA ATTCGCGTTA AATTTTTGTT AAATCAGCTC ATTTTTTAAC
           AAAACAATTT TAAGCGCAAT TTAAAAACAA TTTAGTCGAG TAAAAAATTG

f1 origin
2101   CAATAGGCCG AAATCGGCAA AATCCCTTAT AAATCAAAAG AATAGACCGA
           GTTATCCGGC TTTAGCCGTT TTAGGGAATA TTTAGTTTTC TTATCTGGCT

f1 origin
2151   GATAGGGTTG AGTGTTGTTC CAGTTTGGAA CAAGAGTCCA CTATTAAAGA
           CTATCCCAAC TCACAACAAG GTCAAACCTT GTTCTCAGGT GATAATTTCT

f1 origin
2201   ACGTGGACTC CAACGTCAAA GGGCGAAAAA CCGTCTATCA GGGCGATGGC
           TGCACCTGAG GTTGCAGTTT CCCGCTTTTT GGCAGATAGT CCCGCTACCG

f1 origin
T->A
2251   CCACTACGAG AACCATCACC CTAATCAAGT TTTTTGGGGT CGAGGTGCCG
           GGTGATGCTC TTGGTAGTGG GATTAGTTCA AAAAACCCCA GCTCCACGGC

f1 origin
2301   TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCGATTT AGAGCTTGAC
           ATTTCGTGAT TTAGCCTTGG GATTTCCCTC GGGGGCTAAA TCTCGAACTG

f1 origin
2351   GGGGAAAGCC GGCGAACGTG GCGAGAAAGG AAGGGAAGAA AGCGAAAGGA
           CCCCTTTCGG CCGCTTGCAC CGCTCTTTCC TTCCCTTCTT TCGCTTTCCT

f1 origin
2401   GCGGGCGCTA GGGCGCTGGC AAGTGTAGCG GTCACGCTGC GCGTAACCAC
           CGCCCGCGAT CCCGCGACCG TTCACATCGC CAGTGCGACG CGCATTGGTG

f1 origin
NheI
2451   CACACCCGCC GCGCTTAATG CGCCGCTACA GGGCGCGTGC TAGCCATGTG
           GTGTGGGCGG CGCGAATTAC GCGGCGATGT CCCGCGCACG ATCGGTACAC

f1 origin   ColEI
2501   AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG
           TCGTTTTCCG GTCGTTTTCC GGTCCTTGGC ATTTTTCCGG CGCAACGACC

ColEI
ORI
2551   CGTTTTTCCA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC
           GCAAAAGGT ATCCGAGGCG GGGGGACTGC TCGTAGTGTT TTTAGCTGCG

ColEI
2601   TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT
           AGTTCAGTCT CCACCGCTTT GGGCTGTCCT GATATTTCTA TGGTCCGCAA

ColEI
2651   TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA

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AGGGGGACCT TCGAGGGAGC ACGCGAGAGG ACAAGGCTGG GACGGCGAAT

ColEI

mutation

2701   CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAT
       GGCCTATGGA CAGGCGGAAA GAGGGAAGCC CTTCGCACCG CGAAAGAGTA

ColEI

mutation

2751   AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT
       TCGAGTGCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTCGA

ColEI

mutation

2801   GGGCTGTGTG CACGAACCCC CCGTTCAGTC CGACCGCTGC GCCTTATCCG
       CCCGACACAC GTGCTTGGGG GGCAAGTCAG GCTGGCGACG CGGAATAGGC

ColEI

2851   GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG
       CATTGATAGC AGAACTCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC

ColEI

2901   GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC
       CGTCGTCGGT GACCATTGTC CTAATCGTCT CGCTCCATAC ATCCGCCACG

ColEI

mutation

2951   TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGAACAG
       ATGTCTCAAG AACTTCACCA CCGGATTGAT GCCGATGTGA TCTTCTTGTC

ColEI

mutation

3001   TATTTGGTAT CTGCGCTCTG CTGTAGCCAG TTACCTTCGG AAAAAGAGTT
       ATAAACCATA GACGCGAGAC GACATCGGTC AATGGAAGCC TTTTTCTCAA

ColEI

3051   GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT
       CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA

ColEI

3101   TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC
       ACAAACGTTC GTCGTCTAAT GCGCGTCTTT TTTTCCTAGA GTTCTTCTAG

ColEI

3151   CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAACTCACGT
       GAAACTAGAA AAGATGCCCC AGACTGCGAG TCACCTTGCT TTTGAGTGCA

ColEI

cat terminator

BglII

3201   TAAGGGATTT TGGTCAGATC TAGCACCAGG CGTTTAAGGG CACCAATAAC
       ATTCCCTAAA ACCAGTCTAG ATCGTGGTCC GCAAATTCCC GTGGTTATTG

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         ColEI
         cat terminator
         ‿‿‿‿‿‿‿‿‿
   3251  TGCCTTAAAA AAATTACGCC CCGCCCTGCC ACTCATCGCA GTACTGTTGT
         ACGGAATTTT TTTAATGCGG GGCGGGACGG TGAGTAGCGT CATGACAACA
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3301  AATTCATTAA GCATTCTGCC GACATGGAAG CCATCACAAA CGGCATGATG
         TTAAGTAATT CGTAAGACGG CTGTACCTTC GGTAGTGTTT GCCGTACTAC
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3351  AACCTGAATC GCCAGCGGCA TCAGCACCTT GTCGCCTTGC GTATAATATT
         TTGGACTTAG CGGTCGCCGT AGTCGTGGAA CAGCGGAACG CATATTATAA
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3401  TGCCCATAGT GAAAACGGGG GCGAAGAAGT TGTCCATATT GGCTACGTTT
         ACGGGTATCA CTTTTGCCCC CGCTTCTTCA ACAGGTATAA CCGATGCAAA
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3451  AAATCAAAAC TGGTGAAACT CACCCAGGGA TTGGCTGAGA CGAAAAACAT
         TTTAGTTTTG ACCACTTTGA GTGGGTCCCT AACCGACTCT GCTTTTTGTA
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3501  ATTCTCAATA AACCCTTTAG GGAAATAGGC CAGGTTTTCA CCGTAACACG
         TAAGAGTTAT TTGGGAAATC CCTTTATCCG GTCCAAAAGT GGCATTGTGC
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3551  CCACATCTTG CGAATATATG TGTAGAAACT GCCGGAAATC GTCGTGGTAT
         GGTGTAGAAC GCTTATATAC ACATCTTTGA CGGCCTTTAG CAGCACCATA
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3601  TCACTCCAGA GCGATGAAAA CGTTTCAGTT TGCTCATGGA AAACGGTGTA
         AGTGAGGTCT CGCTACTTTT GCAAAGTCAA ACGAGTACCT TTTGCCACAT
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3651  ACAAGGGTGA ACACTATCCC ATATCACCAG CTCACCGTCT TTCATTGCCA
         TGTTCCCACT TGTGATAGGG TATAGTGGTC GAGTGGCAGA AAGTAACGGT
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3701  TACGGAACTC CGGGTGAGCA TTCATCAGGC GGGCAAGAAT GTGAATAAAG
         ATGCCTTGAG GCCCACTCGT AAGTAGTCCG CCCGTTCTTA CACTTATTTC
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3751  GCCGGATAAA ACTTGTGCTT ATTTTTCTTT ACGGTCTTTA AAAAGGCCGT
         CGGCCTATTT TGAACACGAA TAAAAGAAA TGCCAGAAAT TTTTCCGGCA
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3801  AATATCCAGC TGAACGGTCT GGTTATAGGT ACATTGAGCA ACTGACTGAA
         TTATAGGTCG ACTTGCCAGA CCAATATCCA TGTAACTCGT TGACTGACTT
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3851  ATGCCTCAAA ATGTTCTTTA CGATGCCATT GGGATATATC AACGGTGGTA
         TACGGAGTTT TACAAGAAAT GCTACGGTAA CCCTATATAG TTGCCACCAT
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿
                        CM(R)
   3901  TATCCAGTGA TTTTTTTCTC CATTTTAGCT TCCTTAGCTC CTGAAAATCT
         ATAGGTCACT AAAAAAAGAG GTAAAATCGA AGGAATCGAG GACTTTTAGA
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿     ‿‿‿‿‿‿
            CM(R)              SD
         ‿‿‿‿‿‿‿‿‿‿‿‿‿‿‿         ‿‿
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cat promoter

3951   CGATAACTCA AAAAATACGC CCGGTAGTGA TCTTATTTCA TTATGGTGAA
           GCTATTGAGT TTTTTATGCG GGCCATCACT AGAATAAAGT AATACCACTT

5

cat promoter
CRP site

4001   AGTTGGAACC TCACCCGACG TCTAATGTGA GTTAGCTCAC TCATTAGGCA
           TCAACCTTGG AGTGGGCTGC AGATTACACT CAATCGAGTG AGTAATCCGT

10

cat promoter

lac mRNA start
~
lac operator

15

-35 region   -10 region

4051   CCCCAGGCTT TACACTTTAT GCTTCCGGCT CGTATGTTGT GTGGAATTGT
           GGGGTCCGAA ATGTGAAATA CGAAGGCCGA GCATACAACA CACCTTAACA

20   lac operator   SD   lacZ′

4101   GAGCGGATAA CAATTTCACA CAGGAAACAG CTATGACCAT GATTACGAAT
           CTCGCCTATT GTTAAAGTGT GTCCTTTGTC GATACTGGTA CTAATGCTTA
           lacZ′

25   ~
4151   T
      A

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Figure 30

VL

Restriction sites noted: EcoRV (positions 1–2), BanII (positions 6–8)

Position	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8
						BanII									Framework 1			
VLk1 (SEQ ID NO: 61)	GAT	ATC	CAG	ATG	ACC	CAG	AGC	CCG	TCT	AGC	CTG	AGC	GCG	AGC	GTG	GGT	GAT	CGT
MSPro28 (SEQ ID NO:62)	GAT	ATC	CAG	ATG	ACC	CAG	AGC	CCG	TCT	AGC	CTG	AGC	GCG	AGC	GTG	GGT	GAT	CGT
VLk3 (SEQ ID NO: 63)	GAT	ATC	GTG	CTG	ACC	CAG	AGC	CCG	GCG	ACC	CTG	AGC	CTG	AGC	CCG	GGC	GAA	CGT
MSPro24 (SEQ ID NO: 64)	GAT	ATC	GTG	CTG	ACC	CAG	AGC	CCG	GCG	ACC	TCT	AGC	CTG	AGC	CCG	GGC	GAA	CGT
MSPro29 (SEQ ID NO:65)	GAT	ATC	GTG	CTG	ACC	CAG	AGC	CCG	GCG	ACC	TCT	AGC	CTG	AGC	CCG	GGC	GAA	CGT
VLk4 (SEQ ID NO:66)	GAT	ATC	GTG	ATG	ACC	CAG	AGC	CCG	GAT	AGC	CTG	GCG	GTG	AGC	CTG	GGC	GAA	CGT
MSPro21 (SEQ ID NO:67)	GAT	ATC	GTG	ATG	ACC	CAG	AGC	CCG	GAT	AGC	CTG	GCG	GTG	GCG	CTG	GGC	GAA	CGT
VLl2 (SEQ ID NO:68)	GAT	ATC	GCA	CTG	ACC	CAG	CCA	GCT	.	TCA	GTG	AGC	GGC	TCA	CCA	GGT	CAG	AGC
MSPro55 (SEQ ID NO:69)	GAT	ATC	GCA	CTG	ACC	CAG	CCA	GCT	.	TCA	GTG	AGC	GGC	TCA	CCA	GGT	CAG	AGC
MSPro11 (SEQ ID NO:70)	GAT	ATC	GCA	CTG	ACC	CAG	CCA	GCT	.	TCA	GTG	AGC	GGC	TCA	CCA	GGT	CAG	AGC
MSPro26 (SEQ ID NO:71)	GAT	ATC	GCA	CTG	ACC	CAG	CCA	GCT	.	TCA	GTG	AGC	GGC	TCA	CCA	GGT	CAG	AGC
VLl3 (SEQ ID NO:72)	GAT	ATC	GAA	CTG	ACC	CAG	CCG	CCT	.	TCA	GTG	AGC	GTT	GCA	CCA	GGT	CAG	ACC
MSPro54 (SEQ ID NO: 73)	GAT	ATC	GAA	CTG	ACC	CAG	CCG	CCT	.	TCA	GTG	AGC	GTT	GCA	CCA	GGT	CAG	ACC
MSPro2 (SEQ ID NO:74)	GAT	ATC	GAA	CTG	ACC	CAG	CCG	CCT	.	TCA	GTG	AGC	GTT	GCA	CCA	GGT	CAG	ACC
MSPro12 (SEQ ID NO: 75)	GAT	ATC	GAA	CTG	ACC	CAG	CCG	CCT	.	TCA	GTG	AGC	GTT	GCA	CCA	GGT	CAG	ACC
MSPro59 (SEQ ID NO: 76)	GAT	ATC	GAA	CTG	ACC	CAG	CCG	CCT	.	TCA	GTG	AGC	GTT	GCA	CCA	GGT	CAG	ACC

VH

Restriction site noted: MfeI (positions 3–4)

Position	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8
			MfeI												Framework 1			
VH1A (SEQ ID NO:77)	GAA/CAG	GTG	CAA	TTG	GTT	CAG	TCT	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro21 (SEQ ID NO:78)	CAG	GTG	CAA	TTG	GTT	CAG	TCT	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro24 (SEQ ID NO: 79)	CAG	GTG	CAA	TTG	GTT	CAG	TCT	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro28 (SEQ ID NO: 80)	CAG	GTG	CAA	TTG	GTT	CAG	TCT	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
VH1B (SEQ ID NO: 81)	GAA/CAG	GTG	CAA	TTG	GTT	CAG	AGC	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro54 (SEQ ID NO: 82)	CAG	GTG	CAA	TTG	GTT	CAG	AGC	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro55 (SEQ ID NO: 83)	CAG	GTG	CAA	TTG	GTT	CAG	AGC	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro2 (SEQ ID NO:84)	CAG	GTG	CAA	TTG	GTT	CAG	AGC	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro11 (SEQ ID NO:85)	CAG	GTG	CAA	TTG	GTT	CAG	AGC	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro26 (SEQ ID NO:86)	CAG	GTG	CAA	TTG	GTT	CAG	AGC	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
MSPro29 (SEQ ID NO:87)	CAG	GTG	CAA	TTG	GTT	CAG	AGC	GGC	GCG	GAA	GTG	AAA	AAA	CCG	GGC	AGC	AGC	GTG
VH2 (SEQ ID NO:88)	GAA/CAG	GTG	CAA	TTG	AAA	GAA	AGC	GGC	CCG	GGC	CTG	GTG	AAA	CCG	GCG	CAA	ACC	CTG
MSPro12 (SEQ ID NO:89)	CAG	GTG	CAA	TTG	AAA	GAA	AGC	GGC	CCG	GGC	CTG	GTG	AAA	CCG	GCG	CAA	ACC	CTG
VH6 (SEQ ID NO:90)	GAA/CAG	GTG	CAA	TTG	GTG	CAG	TCT	GGT	GGC	GGC	CTG	GTG	AAA	CCG	GCG	CAA	ACC	CTG
MSPro59 (SEQ ID NO:91)	CAG	GTG	CAA	TTG	GTG	CAG	TCT	GGT	GGC	GGC	CTG	GTG	AAA	CCG	GCG	CAA	ACC	CTG

CDR 1

Framework and CDR 1 codon table (top). Column positions are numbered (…19 20 … 30 a b c d e f … 38). Restriction‑enzyme sites indicated: **PstI** (columns 2–4 region), **KpnI** (columns 5–7 region).

20	19	1	2	3	4	5	6	7	8	9	30	a	b	c	d	e	f	1	2	3	4	5	6	7	8
GTG	ACC	ATT	ACC	TGC	AGA	GCG	AGC	CAG	GGC	ATT	AGC	–	–	–	–	–	–	TAT	CTG	GCG	TGG	TAC	CAG	CAG	
GTG	ACC	ATT	ACC	TGC	AGA	GCG	AGC	CAG	GGC	ATT	AGC	–	–	–	–	–	–	TAT	CTG	GCG	TGG	TAC	CAG	CAG	
GCG	ACC	AGC	ACC	TGC	AGA	GCG	AGC	CAG	GGC	AGC	AGC	–	–	–	–	–	–	TAT	CTG	GCG	TGG	TAC	CAG	CAG	
GCG	ACC	AGC	ACC	TGC	AGA	GCG	AGC	CAG	AGC	GTG	AGC	AGC	–	–	–	–	–	TAT	CTG	GCG	TGG	TAC	CAG	CAG	
GCG	ACC	CTG	ACC	TGC	AGA	GCG	AGC	CAG	AGC	GTG	AGC	AAC	AAC	–	–	–	–	TAT	CTG	GCG	TGG	TAC	CAG	CAG	
GCG	ACC	CTG	ACC	TGC	AGA	GCG	AGC	CAG	AGC	GTG	AGC	AAC	AAC	–	–	–	–	TAT	CTG	GCG	TGG	TAC	CAG	CAG	
GCG	ACC	ATT	ACC	TGC	AAC	GCG	AGC	CTG	AGC	GTG	GAT	TAT	AAC	AAA	–	–	–	TAT	CTG	AGC	TGG	TAC	CAG	CAG	
GCG	ACC	ATT	ACC	TGC	AAC	GCG	AGC	CTG	AGC	GTG	GAT	TAT	AAC	AAA	–	–	–	TAT	CTG	AGC	TGG	TAC	CAG	CAG	
ATT	ACC	ATC	TCG	TGT	AGC	AGC	GGT	GTG	GTG	GGC	GGC	GGC	TAT	AAA	AAC	–	–	TAT	GCG	AGC	TGG	TAC	CAG	CAG	
ATT	ACC	ATC	TCG	TGT	AGC	AGC	GGT	GTG	GTG	GGC	GGC	GGC	TAT	AAA	AAC	–	–	TAT	GCG	AGC	TGG	TAC	CAG	CAG	
ATT	ACC	ATC	TCG	TGT	AGC	AGC	GGT	GTG	CTG	GGC	GGC	GGC	TAT	AAA	AAA	–	–	GCG	GCG	AGC	TGG	TAC	CAG	CAG	
ATT	ACC	ATC	TCG	TGT	AGC	AGC	GGT	GTG	CTG	GGC	GGC	GGC	GAT	AAA	AAA	–	–	GCG	GCG	AGC	TGG	TAC	CAG	CAG	
GCG	CGT	ATC	TCG	TGT	AGC	AGC	GGC	CTG	CTG	GGC	GGC	GAT	AAA	–	–	–	–	GCG	GCG	AGC	TGG	TAC	CAG	CAG	
GCG	CGT	ATC	TCG	TGT	AGC	AGC	GCG	CTG	CTG	GGC	GGC	GAT	AAA	–	–	–	–	TAC	GCG	AGC	TGG	TAC	CAG	CAG	
GCG	CGT	ATC	TCG	TGT	AGC	AGC	GCG	CTG	CTG	GGC	GGC	GAT	AAA	–	–	–	–	TAC	GCG	AGC	TGG	TAC	CAG	CAG	
GCG	CGT	ATC	TCG	TGT	AGC	AGC	GCG	CTG	CTG	GGC	GGC	GAT	AAA	–	–	–	–	TAC	GCG	AGC	TGG	TAC	CAG	CAG	

CDR 1   **Frame**

Framework and CDR 1 codon table (bottom). Restriction‑enzyme sites indicated: **BspEI** (TCC GGA), **BstXI**.

20	19	1	2	3	4	5	6	7	8	9	30	1	a	b	2	3	4	5	6	7	8	9	0	1	2
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	GGC	ACT	TTT	AGC	AGC	–	–	TAT	GCG	ATT	AGC	TGG	GTG	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	GGC	ACT	TTT	AGC	AGC	–	–	TAT	GCG	ATT	AGC	TGG	GTG	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	GGC	ACT	TTT	AGC	AGC	–	–	TAT	GCG	ATT	AGC	TGG	GTG	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	GGC	ACT	TTT	AGC	AGC	–	–	TAT	GCG	ATT	AGC	TGG	GTG	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	GGC	ACC	TTT	ACC	AGC	–	–	TAT	GCG	ATT	CAC	TGG	GTC	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	TAT	ACC	TTT	ACC	AGC	–	–	TAT	TAT	ATG	CAC	TGG	GTC	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	TAT	ACC	TTT	ACC	AGC	–	–	TAT	TAT	ATG	CAC	TGG	GTC	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	TAT	ACC	TTT	ACC	AGC	–	–	TAT	TAT	ATG	CAC	TGG	GTC	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	TAT	ACC	TTT	ACC	AGC	–	–	TAT	TAT	ATG	CAC	TGG	GTC	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	TAT	ACC	TTT	ACC	AGC	–	–	TAT	TAT	ATG	CAC	TGG	GTC	CGC	CAA	CGC	CCT	GGG
AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	TAT	ACC	TTT	ACC	AGC	–	–	TAT	TAT	GGC	GGC	TGG	ATT	CGC	CAG	CGC	CCT	GGG
AAA	GTG	AGC	TGC	ACC	TCC	TCC	GGA	TTT	CTG	TCC	ACG	AGC	–	–	GGC	TAT	GGC	GGC	TGG	ATT	CGC	CAG	CGC	CCT	GGG
ACC	CTG	ACC	TGT	ACC	TTT	TCC	GGA	TTT	CTG	TCC	ACG	AGC	–	–	GGC	TAT	GGC	GTG	GGC	AAC	CGC	CAG	CGC	CCG	GGG
ACC	CTG	ACC	TGT	GCG	ATT	TCC	GGA	GAT	GTG	GCG	AGC	AGC	–	–	GCG	GCG	GCG	TGG	TGG	AAC	CAG	CGC	CCG	TCT	GGG
AGC	CTG	ACC	TGT	GCG	ATT	TCC	GGA	GAT	GTG	GCG	AGC	AGC	–	–	GCG	GCG	GCG	AAC	TGG	AAC	CAG	CGC	CGC	CCT	GGG

SUBSTITUTE SHEET (RULE 26)

Top table — Framework 2 / CDR 2

Restriction sites: SexAI · AseI · SanDI

Kabat positions (left → right): 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73

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AAA CCA GGT AAA GCA AAA CCG CTA TTA ATT TAT GCA GCC AGC TTG CAA AGC GGG GTC CCG TCC CGT TTT AGC GGC
AAA CCA GGT AAA GCA AAA CCG CTA TTA ATT TAT GCA GCC AGC TTG CAA AGC GGG GTC CCG TCC CGT TTT AGC GGC
AAA CCA GGT CAA GCA CGT CCG CTA TTA ATT TAT GGC GCC AGC CGT GCA AGC GGG GTC CCG GCG CGT TTT AGC GGC
AAA CCA GGT CAA GCA CGT CCG CTA TTA ATT TAT GGC GCC AGC CGT GCA ACT GGG GTC CCG GCG CGT TTT AGC GGC
AAA CCA GGT CAA GCA CGT CCG CTA TTA ATT TAT GGC GCC AGC CGT GCA ACT GGG GTC CCG GCG CGT TTT AGC GGC
AAA CCA GGT CAA GCA CGT CCG CTA TTA ATT TAT GGC GCC AGC CGT GCA ACT GGG GTC CCG GCG CGT TTT AGC GGC
AAA CCA GGT CAG CCG AAA CCG CTA TTA ATT TAT TGG GCA TCC ACC TCC AGC GGG GTC CCG GAT CGT TTT AGC GGA
AAA CCA GGT CAG CCG AAA CCG CTA TTA ATT TAT TGG GCA TCC ACC TCC AGC GGG GTC CCG GAT CGT TTT AGC GGA
CAT CCC GGG AAG GCG AAA CCG CTG ATG ATT TAT GAT GTG AGC AAC AGC TCA GGC GTG AGC AAC AAC TTT AGC GGA
CAT CCC GGG AAG GCG AAA CCG CTG ATG ATT TAT GAT GTG AGC AAC AGC TCA GGC GTG AGC AAC AAC TTT AGC GGA
CAT CCC GGG AAG GCG AAA CCG CTG ATG ATT TAT GAT GTG AGC AAC AGC TCA GGC GTG AGC AAC AAC TTT AGC GGA
CAT CCC GGG AAG GCG AAA CCG CTG ATG ATT TAT GAT GTG AGC AAC AGC TCA GGC GTG AGC AAC AAC TTT AGC GGA
AAA CCC GGG CAG GCG CCG CCA CTG GTG ATT TAT GAT GAT TCT GAC CGT TCA GGC ATC CCG GAA CGC TTT AGC GGA
AAA CCC GGG CAG GCG CCG CCA CTG GTG ATT TAT GAT GAT TCT GAC CGT TCA GGC ATC CCG GAA CGC TTT AGC GGA
AAA CCC GGG CAG GCG CCG CCA CTG GTG ATT TAT GAT GAT TCT GAC CGT TCA GGC ATC CCG GAA CGC TTT AGC GGA
AAA CCC GGG CAG GCG CCG CCA CTG GTG ATT TAT GAT GAT TCT GAC CGT TCA GGC ATC CCG GAA CGC TTT AGC GGA
AAA CCC GGG CAG GCG CCG CCA CTG GTG ATT TAT GAT GAT TCT GAC CGT TCA GGC ATC CCG GAA CGC TTT AGC GGA
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Bottom table — Framework 2 / CDR 2

Restriction site: XhoI

Positions (left → right): 33 34 35 36 37 38 39 50 51 52 a b c 53 54 55 56 57 58 59 60 61 62 63 64 65

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CAG GGT CTC GAG TGG ATG GGC ATT ATT CCG  -   -   -  ATT TTT GGC GCG AAC GCG GCG TAC GCG CAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC ATT ATT CCG  -   -   -  ATT TTT GGC GCG AAC GCG GCG TAC GCG CAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC ATT ATT CCG  -   -   -  ATT TTT GGC GCG AAC GCG GCG TAC GCG CAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC ATT ATT CCG  -   -   -  AAT AGC GGC GCG GGC ACG GCG TAC GCG CAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC ATT ATT CCG  -   -   -  AAT AGC GGC GGC GGC ACG GCG TAC GCG CAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC ATT ATT CCG  -   -   -  AAT AGC GGC GGC GGC ACG GCG TAC GCG CAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC TGG ATT AAC  -   -   -  AAT AGC GGC GGC GGC ACG TAC TAC GCG CAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC TGG ATT AAC  -   -   -  AAT AGC GGC GGC GGC ACG TAC TAC GCG CAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC TGG ATT AAC  -   -   -  AAT AGC GGC GGC GGC ACG TAC TAC GCG CAG AAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC TGG ATT AAC  -   -   -  AAT AGC GGC GGC GGC AAG TAC TAC GCG CAG AAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC TGG ATT AAC  -   -   -  AAT AGC GGC GGC GGC AAG TAC TAC GCG CAG AAG TTT CAG GGC
CAG GGT CTC GAG TGG ATG GGC TGG ATT AAC  -   -   -  AGC AGC GGC GGC AAC AAG TAT TAT GAT GCG CAG AAG TTT CAG GGC
AAA GCC CTG GCT CGT ACC TAT TAT CGT  -   -   -  TGG AAA GAT GAT TGG GGC AAA AGC
AAA GCC CTG GCT CGT ACC TAT TAT CGT  -   -   -  TGG AAA GAT GAT TGG GGC AAA AGC
CGT GGC GGC CTG GGC TAT TAT AGC  -   -   -  AGC GAT GTG GCG GTG AGC
CGT GGC GGC CTG GGC TAT TAT AGC  -   -   -  AGC GAT GTG GCG GTG AGC
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Framework 3

BamHI

BbsI

Framework 3

BstEII

NspV

Framework 4

CDR 3

BsiWI

MscI

CDR 3

BssHII

EagI

j	k	1	1	2	3	4	5	6	7	8	9	0	1	2	3
						StyI						11		BlpI	
x	x	x	GAT	x	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
CCT	TTT	TCT	GAT	GTT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
TAT	ACT	TTT	GAT	TAT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
TAT	CTT	TTT	GAT	CTT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
x	x	x	GAT	x	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
CCT	CAT	TTT	GAT	TAT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
GTT	CTT	TTT	GAT	CAT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
TAT	GAG	TTT	GAT	TAT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
GGT	TTT	ATT	GAT	TAT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
GGT	TAT	TTT	GAT	AAT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
TAT	TAT	TTT	GAT	ATT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
x	x	x	GAT	x	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
TAT	ATG	TTT	GAT	TAT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
x	x	x	GAT	x	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC
CCT	GAT	TTT	GAT	TAT	TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	GC

Framework 4